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AAU12175
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Copyright (c) 1993 - 2000 Compugen Ltd
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50
                                                        DFMIQGGDF 9
                                                                  BLOSUM62
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Perfect score: Scoring table:

Sequence:

Searched:

OM protein

Run on:

## ALIGNMENTS

human; tumour antigen peptide; cytotoxic T-cell; CTL; Tumour antigen peptides derived from cyclophilin B for treatment and diagnosis of tumours  $\,\cdot\,$ Human cyclophilin B peptide fragment #2. HLA antigen; diagnosis; tumour; therapy AAY69922 standard; peptide; 9 AA. SUMU ) SUMITOMO PHARM CO LID. 98JP-0178449. 99WO-JP03360. (first entry) WPI; 2000-116932/10. Itoh K, Gomi S; ITOH K. Cyclophilin B; WO9967288-A1. Homo sapiens. 24-JUN-1999; 11-APR-2000 25-JUN-1998; 29-DEC-1999 AAY69922; (ITOH/) RESULT AAY69922 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Carboak gradata/geneseq/geneseqp/AA1980\_DAT:\*
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| SIDS8/gradata/geneseq/geneseqp/AA1991\_DAT:\*

A\_Geneseq\_1101:\*

Database

		Description	wilidao(ovo demaH	Human cyclonhilin	Himan secreted ord	Human prostate can	Himan Cvolonbilin	Cyclophilin C M:	A night pentidul-	Human Cyclophilin	Arabidonsis thalia	Arabidopsis thalia	Arabidopsis thalia	
SOMMARIES		Ð	AAY69922	AAB46931	AAG00090	AAB56701	AAB73302	AAR32353	AAY92048	AAB73301	AAG16463	AAG05073	AAG16462	
		80	21	22	21	21	22	14	21	22	21	21	21	
		Match Length DB	6	0	166	183	211	212	212	216	252	254	254	
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Claim 4; Page 49; 64pp; Japanese

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Query Match
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Matches 9; Conserv
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AABS6701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes the novel use of interferons (IFNs) or DNas capable of expressing the interferons and/or antigenic proteins (AP), antigenic peptides derived from the proteins or DNas capable of expressing the antigenic proteins or peptides, in the manufacture of an agent for induction of antigen-specific T cells. The products of the Invention have virucide and cytostatic activity and can be used for gene therapy or as inducers of antigen-specific T cells. The action of interferon-alpha (IEN-alpha) in a system for inducing specific cytotoxic r cell (CTL) by administering an antigenic peptide in an incomplete Freund's adjuvant (IFN) emission preparation form was evaluated. IFNs (DNA encoding IFNs) are useful in the manufacture of a medicament for inducing antigen-specific T cells in an individual who has been administered with AP (or DNA encoding AP) or vice versa. The medicament is useful for the treatment or prophylaxis of a tumor or a viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of antigenic proteins, peptides, interferon or their encoding DNA, in the manufacture of an agent for the induction of antigen-specific {\bf T}
             This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                         Tumor antigenic peptide: interferon; IFN; antigen-specific T cell; virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell; viral infectious disease; cyclophilin B; human.
                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                 Human cyclophilin B derived tumor antigenic peptide SEQ ID 17.
                                                                                                                   Query Match 100.0%; Score 50; DB 21; Length 9; Best Local Similarity 100.0%; Pred. No. 4.3e+05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 15; 25pp; English.
                                                                                                                                                                                                                                                                     AAB46931 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takasu H, Gotoh M, Yamaoka T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUMU ) SUMITOMO PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99JP-0207687.
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                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                            1 DFMIQGGDF 9
                                                                                                                                                                                          9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo saplens
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                                                                                                                                                                                                                                                                                               AAB46931;
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AAB46931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a polypeptide encoded by one of a large number of 5 ESTS derived from mRNAs encoding secreted proteins. The 5 ESTS were prepared from total human RNAs or poly4+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3 untranslated region (UTR) of the mRNA because they are often obtained from oligo-dry primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intact 5' of the and send sand can therefore be used to obtain full length cDNAs and genomic buns. 5' ESTS are also used in diagnostic, forensic, gene therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
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Score 50; DB 22;
Pred. No. 4.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; SEQ ID 4171; 71pp + CD-ROM; English.
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                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein, SEQ ID NO: 4171.
                                                                                                                                                                                                                                                                                                               AAG00090 standard; Protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; chromosome mapping.
   100.0%;
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                                                            9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dfmiqggdf 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                      AAG00090;
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somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteoporosis; HIV infection; breast cancer; gigantism; acromegaly; hyperprolactinaemia; C-terminal deletion mutant; mutefin. Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding;

10-AUG-2000; 2000WO-US21789

WO200113113-A1

22-FEB-2001

Homo sapiens.

99US-0149752.

19-AUG-1999;

Rycyzyn MA;

Clevenger CV,

WPI; 2001-211249/21

(UYPE-) UNIV PENNSYLVANIA.

Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.

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neuroprotective, cytostatic; cardioactive, immunomodulatory, muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulnonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used for detection of prostate cancer, chromosome polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and prolliferative disorders, wounds, and infectious diseases. AAR16506 to AAR16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                        Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                       Human prostate cancer antigen protein sequence SEQ ID NO:1279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 1699-1700; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              disorders such as prostate cancer
AAB56701 standard; Protein; 183
                                                                                                                                                                                                                                                                                                          HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                         08-MAR-2000; 2000WO-US05988
                                                                                                                                                                                                                                                                                  99US-0124270
                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                              Rosen CA, Ruben SM
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-587513/55.
N-PSDB; AAF15904.
                                                                                                                                                                                                                                                                                                                      (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 AA;
                                                                                                                                                                                                        WO200055174-A1.
                                                                                                                                                                                    Homo sapiens.
                                               13-MAR-2001
                                                                                                                                                                                                                                                                                 12-MAR-1999;
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Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone

Disclosure; Page -; 21pp; English.

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The invention relates to a composition for modulating somatolactogenic function, comprising cyclophilin B (CypB), a mutant of cyclophilin B (pyB), a mutant of cyclophilin B (PyB), a mutant of cyclophilin B (PyB), a mutant of cyclophilin B contains a comparable of cyclophilin B with a somatolactogenic character to a method of identifying inhibitors of somatolactogenic also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB and a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic hormone, is useful for augmenting somatolactogenic function in the animal, and cyclophilin B mutant or a composition comprising cyclophilin B is useful in the treatment of immunosuppression, of the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprising cyclophilin and because and processes.

C hormone, is useful for treating HIV infection, breast and processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer, gigantism/acromegaly, and hyperprolactinaemia. The present sequence represents a human cyclophilin B C-terminal mutant, CypB-AIAKE. Note: The present sequence is not shown in the specification, but is derived from the wild-type CypB sequence shown on pages 17-18.
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Best Local Similarity 100. Matches 9; Conservative

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1 DFMIQGGDF 9

ò g AAB73302 standard; protein; 211 AA.

AAB73302

22-MAY-2001 (first entry)

AAB73302;

SX SX E

100.0%; Score 50; DB 21; Length 183; 100.0%; Pred. No. 0.2;

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Asperqillus niger.
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                                                                       Protein
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C G. This color was isolated from a substracted sub-library contg.

G Genes induced by treatment of the stromal cell line with interleukin.

I (IL-1). The message levels for cyp C show a 2-3 fold induction by creatment with IL-1, and this color exhow a 2-3 fold induction by with known cyclophilins. Cyp C is distinct from mammalian cyclophilins. Cyp C is distinct from mammalian cyclophilins A and B in both sequence and tissue distribution of cyclophilins A and B in both sequence and tissue distribution of cyclophilins are some section of the mammalian completely inhibited by addition of cyclosporin A (CsA). These cyp C is usion proteins and be used as ligands for the ladentification of intracellular proteins which together form high affinity associations. For example, the cyp C fusion protein binds to a protein of 77 kD in the absence of CsA, while in the presence of CsA it no longer binds to this p77, but instead binds specifically to a protein of 55 kD, identified as calcineurin (U.S.S.N.07/740175).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclophilin-like peptidyl prolyl cis-trans isomerase: CYPB; food processing; Endoplasmic retention signal; cis-trans isomerization; protein secretion: toxin; ADP-glucose pyrophosphorylase; glucanase; beta-1,4-endoglucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                Cyclophilin C; bonc marrow; stromal cell line; AC 6; interleukin-1; IL-1; cyp A; cyp B; peptidyl-prolyl isomerase; PPIase; cyclosporin A; CsA; ligand; calcineurin.
                                                                                                                                                                                                                                                                                                   - useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                   Cyclophilin C polypeptide and nucleic acid encoding it for screening a tissue-specific immunosuppressive agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A. niger peptidyl-prolyl cis-trans isomerase (CYPB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 46 + Fig 1; 63pp; English.
                                                                                                                                                                                                               (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY92048 standard; Protein; 212 AA.
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                                                                                                                                                             92WO-US06462
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                                                                                                                                                                                                                                       Weissman IL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
'-has 9; Conserve
                                                                                                                                                                                                                                                              WPI; 1993-076431/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 AA;
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             Cyclophilin C.
                                                                                                                                                                                                                                       Friedman JS,
                                                                                     Mus musculus
                                                                                                                                                              05-AUG-1992;
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                                                                                                             WO9303050-A.
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LID AAY9
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KW Cycl
KW Cycl
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This sequence shows Aspergillus niger cyclophilin-like peptidyl prolyl cis-trans isomerase (CYPB). CYPB is capable of catalyzing the cis-trans isomerase (CYPB). CYPB is capable of catalyzing the cis-trans isometization of a peptide bond on the N-terminal side of proline residues in polypeptides. CYPB are useful in methods for increasing the yield of secreted polypeptides from cells. The secreted polypeptides may be enzymes (such as chymosin, thaumatin or alpha-galactosidase) that can be used in food processing, a pest toxin, adenosine diphosphate (ADP)-glucose pyrophosphorylase, a glucanase or beta-1,4-endoglucanase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptidyl prolyl cis-trans isomerase, designated CYPB, from Aspergillus niger, useful in methods for increasing the yield of secreted polypeptides, such as enzymes used in food processing, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                               /label= signal_peptide
24..212
                                                                                                                                           /label- mature_protein
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Location/Qualifiers
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N-PSDB; AAA08772.
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Best Local Similarity
Matches 9; Conserv
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990S-0132863.
990S-0134256.
990S-0134218.
990S-0134219.
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99US-0137724.
99US-0138094.
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990S-0139461
990S-0139463
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990S-0139817
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990S-0135353.
990S-0135629.
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99US-0142055.
99US-0142390.
99US-0142803.
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990S-0127462.
990S-0128234.
550S-0128714.
990S-0129845.
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99US-0132407.
99US-0132484.
99US-0123548.
99US-0125788.
99US-0126264.
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99US-0143624
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  The invention relates to a composition for modulating somatolactogenic function, comprising cyclophilin B (CypB), a mutant of cyclophilin B (particularly a CypB mutant in which residues 2-12 of the mature protein care absent) or an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone (e.g., prolactin, growth hormone). The invention also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB levels in a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic function in the animal, and cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic function in the animal. A composition comprising cyclophilin B is useful in the treatment of immunosuppression, in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprising cyclophilin B mutant or a composition comprising cyclophilin B with a somatolactogenic composition comprising cyclophilin B with a somatolactogenic connone, is useful for treatment of interaction of cyclophilin B with a somatolactogenic connone, its useful for treating HIV infection, breast and prostate cancer, gigantism/acromegaly, and hyperprolactinaemia. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                   Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 100.0%; Score 50; DB 22; Length 216; Best Local Similarity 100.0%; Pred. No. 0.24; Matches 9; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                  Claim 1; Page 17-18; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-2000; 2000EP-0301439.
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10-AUG-2000; 2000WO-US21789
                        99US-0149752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-2000 (first entry)
                                               (UYPE-) UNIV PENNSYLVANIA.
                                                                      Clevenger CV, Rycyzyn MA;
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                                                                                             WPI; 2001-211249/21.
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                       19-AUG-1999;
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05-MAR-1999;
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PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144008.
PR 19-JUL-1999; 99US-0144088.
PR 19-JUL-1999; 99US-0144328.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144331.
PR 20-JUL-1999; 99US-0144331.
PR 21-JUL-1999; 99US-0144612.
PR 22-JUL-1999; 99US-0144612.
PR 22-JUL-1999; 99US-0144612.
PR 22-JUL-1999; 99US-014612.
PR 22-JUL-1999; 99US-014612.
PR 22-JUL-1999; 99US-014612.
PR 22-JUL-1999; 99US-014612.
PR 22-JUL-1999; 99US-014613.
PR 23-JUL-1999; 99US-014613.
PR 23-JUL-1999; 99US-014613.
PR 23-RUC-1999; 99US-015618.
PR 23-
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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Local Similarity 100.0%;
les 9; Conservative 0
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05-MAR-1999;
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25-MAR-1999;
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5-0130449. 5-0130510. 5-0130891.	-01314	-01324 -01324	3-01324 3-01324	3-01324 3-01328	-01342	3-01342	3-01342	-01347	3-01349 3-01351	3-01353	3-01360	3-01363	-01372	5-013/5 5-01375	3-01377	5-01380 5-01385	5-01388	3-01394	5-01394	5-01394	5-01394 5-01394	5-01394 3-01394	5-01394	3-01394 3-01394	3-01394	5-01394 5-01397	3-01397 3-01398	5-01398	5-01403 3-01403	5-01406	5-01408 5-01409	5-01412	5-01421	3-01 <b>4</b> 20 3-01423	5-01428	5-01429 5-01429	5-01435	S-01436 S-01440	5-01440	5-01440 5-01443	5-01443
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1100001	-1999; -1999;	-1999; -1999;	-1999; -1999;	1999;	1999;	-1999;	1999;	-1999;	-1999;	-1999;	-1999;	-1999;	-1999;	-1999;	-1999;	-1999;	-1999;	1999;	-1999;	1999;	-1999;	-1999;	-1999;	-1999; -1999;	-1999;	1999;	-1999;	-1999;	-1999;	-1999;	-1999;	-1999;	-1999;	-1999;	-1999;	-1999; -1999;	-1999;	-1999; -1999;	-1999;	-1999;	-1999;
23-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999;	28-APR	30-APR	05-MAY 06-MAY	06-MAY	11-MAY	14 - MAY	14 - MAY	18-MAY	19-MAY 20-MAY	21-MAY	25-MAY	27 - MAY	01-JUN	04-JUN	NUT- 70	10-30N	10-JUN	16-JUN	16-JUN	18-JUN	18-JUN	18-JUN	18-JUN	18-JUN 18-JUN	18-JUN	18-30N	18-JUN	22-JUN	23-JUN	24 - JUN	29-JUN	30-JUN	01-JUL 01-JUL	02-JUL 06-JUL	10F-80	09-JUL 12-JUL	13-JUL	14-JUL 15-JUL	16-JUL	19-30L	19-JUL
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 20-JUL-1999;
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 99US-014508.

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 22-JUL-1999;
 99US-014508.

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990S-0131449.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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14-JUL-1999;
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                                                                                                                                                                                                                18-JUN-1999;
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     ö
                                                                                                                                                                                                                                                                                                                                                                       protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                         Gaps
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                                                                                                                                              100.0%; Score 50; DB 21; Length 259; 100.0%; Pred. No. 0.29;
                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 17117.
                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                AAG16461 standard; Protein; 260 AA.
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990S-0123180.
990S-0125788.
990S-0125788.
990S-0125785.
990S-0127462.
990S-0127462.
990S-0127462.
990S-0129845.
990S-0139845.
990S-0130449.
990S-0131449.
990S-0132484.
990S-0132484.
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990S-0134370.
990S-0134768.
990S-0134941.
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99US-0134218.
99US-0134219.
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99US-0161404.
99US-0161405.
99US-0161359.
99US-0161361.
99US-0161361.
99US-0161363.
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                                                                                                                                                                                                                                                                                                                                17-OCT-2000 (first entry)
                                                                                                                                                     Ouery Match 100.

Best Local Similarity 100.

Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                1 DFMIOGGDF 9
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23 - APR - 1999;
28 - APR - 1999;
30 - APR - 1999;
44 - MAY - 1999;
65 - MAY - 1999;
66 - MAY - 1999;
66 - MAY - 1999;
11 - MAY - 1999;
14 - MAY - 1999;
14 - MAY - 1999;
14 - MAY - 1999;
15 - MAY - 1999;
16 - MAY - 1999;
17 - MAY - 1999;
19 - MAY - 1999;
19 - MAY - 1999;
20 - MAY - 1999;
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06-APR-1999;
08-APR-1999;
16-APR-1999;
19-APR-1999;
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          22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
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AAG16461
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990S-0151438.
990S-0151930.
990S-0152363.
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99US-0150566.
99US-0150884.
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9908-0155486
9908-0156458
9908-0156596
9908-0157753
9908-0157753
9908-0158629
9908-0158629
9908-0158939
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990S-0159329.
990S-0159330.
990S-0159331.
990S-0159637.
        99US-0146389
99US-0147038
                                        99US-0147260
99US-0147303
                           99US-0147302
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                     99US-0147204
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99US-0149175
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99US-0154779
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                  04 - AUG-1999;
04 - AUG-1999;
05 - AUG-1999;
05 - AUG-1999;
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23-AUG-1999;
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28-SEP-1999;
29-SEP-1999;
04-OCT-1999;
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22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
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13-OCT-1999
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31-AUG-1
01-SEP-1
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26-AUG-1
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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB4239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities controlled: Cytostatic; proliferative; vulnerary: Immunomodulator; antidiabetic; antiathmatic; antithermatic; an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiabrematic; antibacterial; canting antinflammatory; antichyroid; antiallery(c; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coaquiant; nootropic; immune disorder; haematopoietic call disorder; autoimmune disorder; haematopoietic call disorder; autoimmune disorder; allery creation; allery creation; garaft versus host disease; organ rejection; neurological disease; drug screening.
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing \alpha, g . cancer
                                                                                                                                                                                       ö
                                                                                                                                      DB 21; Length 260;
                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer associated protein sequence SEQ ID NO:1323.
                                                                                                                                Score 50; DB 21
Pred. No. 0.29;
                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 1974-1975; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 AAB43878 standard; Protein; 291 AA.
                                                                                                                                                                                 0
                                                                                                                                100.0%;
  99US-0161920.
99US-0161992.
99US-0161993.
                                                                            99US-0162142
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                                                                                                                                                                               9; Conservative
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                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                           1 DFMIQGGDF 9
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28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
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                                                                                                                             Query Match
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Matches
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Search completed: January 15, 2002, 13:05:27 Job time: 198 sec

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inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB4240 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The yeast PPIase has the following properties: 1. it isomerises an X-Pro bond in a peptide chain (X = any amino acid); 2. it has single molecular weight about 17,000 (by SDS-PAGE); 3. it has single isoelectric point about 5.2 (by iso-electric focussing) and 4. it is inhibited by cyclosporin A. The enzyme is useful for accelerating protein folding, especially for activating recombinantly produced proteins. The PPIase can be produced in the same cell as the recombinant proteins.
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89JP-0184738.
89JP-0260244.
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Best Local Similarity 88.9
Matches 8; Conservative
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174 dfmiqggdf 182
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06-OCT-1989;
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AARI 0764

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Gaps

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Sequence 8, Appliseduence 13, Appliseduence 6, Appliseduence 6, Appliseduence 6, Appliseduence 6, Appliseduence 5, Appliseduence 5, Appliseduence 5, Appli

Appl Appl Appl Appl

Sequence S sequence

US-08-486-099-88 US-08-360-107A-98

Sequence 5, Al Sequence 5, Al Sequence 5, Al Sequence 13, Al Sequence 13, Al Sequence 13, Al Sequence 13, Al

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GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SECUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flebr, Hebbach, Test, Albritton
ADDRESSEE: Retrier
STREET: Four Embarcadero Center, Suite 3400
CITY: San Prantisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 49; DB 2; Length 12
100.0%; Pred. No. 0.023;
ive 0; Mismatches 0; Indels
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COMPUTER: ITEM PC COMPATIBLE
SOFTWARE: PACHOLIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DARK
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-UN-1995
CLASSIPECATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SILVA, ROBIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
                                                     . Sequence 10, Application US/08482728Å
; Patent No. 5968802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 10:
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amino acid
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ZIP: 94111-4187
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Matches 9; Conservative
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MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                                                                                                   (without alignments)
5.381 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                        January 15, 2002, 13:00:24; Search time 37.64 Seconds
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-482-728A-10
US-08-412-897-5
US-08-112-897-5
US-08-112-897-5
US-08-112-897-5
US-08-112-897-5
US-08-112-897-5
US-09-028-366-4
US-09-028-366-3
US-09-028-366-3
US-08-114-852-3
US-08-114-852-3
US-09-114-852-3
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US-08-415-995A-14
US-08-415-995A-14
US-08-415-995A-14
US-08-415-995A-14
US-08-415-995A-14
US-08-415-995A-14
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                                                                                                                                                                                                                                                                                                                                                      212252 seqs, 22503292 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listing first 45 summaries
                                                                                  OM protein – protein search, using sw mode
                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                           US-09-720-469-1
                                                                                                                                                                                                                                                 1 KFHRVIKDF 9
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Match Length
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                                                                                                                                                                                                         Title:
Perfect score:
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Gaps

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Length 126;

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GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Welssman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
TITLE OF INVENTION: and Uses
TORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STRATE: California
COUNTRY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 100.0%; Score 49; DB 1; Length 208; Best Local Similarity 100.0%; Pred. No. 0.036; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.25
                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
                                                                                                                                                                                              5490A-92-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-142-897-5
; Sequence 5, Application US/08142897
; Patent No. 5447852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 208 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-142-897-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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CLASSIFICATION: 435
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SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KFHRVIKDF 9
                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94105
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APPLICANT: Friedman, Jeffrey S.
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Friedman, Jeffrey S.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
TITLE OF INVENTION: and Uses
ANDRESERS: 10
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESERS: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                       APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Fayan, Donald
TITLE OF INVENTION: no. 5968802el Nuclear Cyclophilin
UNDBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco COMPUTER: IBM PC Compatible COMPUTER: IBM PC COMPATIBLE PC-DOS/MS-DOS SOFTMARE: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: S11va, Robin M.
REGISTRATION NUMBER: 38,304
REFRENCE/DOOKET NUMBER: A-61230/DJB/RMS
TELECOHMUNICATION INFORMATION:
TELERAX: (415) 781-1989
TELERAX: (415) 386-3249
TELERAX: 910 277299
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE GIRARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                               ADDRESSEE: Flehr, Hohbach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/482,728A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INPERMATION:
                                                                                                                     Sequence 11, Application US/08482728A Patent No. 5968802
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08142897
Patent No. 5447852
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Best Local Similarity 100.
Matches 9; Conservative
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MOLECULE TYPE: protein
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35 KFHRVIKDF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KFHRVIKDF 9
35 KFHRVIKDF 43
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5968802el Nuclear Cyclophilin
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TIP: 94111-4187

TIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                      APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclop
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton
ADDRESSEE: Flehr, Hobbach
ADDRESSEE: Flebr, Herbert
SIRRET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REGISTRATION NUMBER: 38,304
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 788-3249
TELEFAX: 910 277299
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
         Pred. No. 0.68;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB;
Pred. No. 2.7;
2; Mismatches
                                                                                                                                                                                                                Sequence 19, Application US/08482728A Patent No. 5968802 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09028366
Patent No. 6150501
      77.88;
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77.88;
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Best Local Similarity 77.8°
         Best Local Similarity 77.8 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-482-728A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||:||:|
320 KFHRLIKNF 328
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32 KFHRLIKNF 40
                                                                   1 KFHRVIKDF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Fisher, Joseph
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INFENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton
ADRESSEE: & Herbert
STREET: Four Embarcadero.Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: US/08/482,728A
FILLING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: S11va, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 38,404
TELECOMMUNICATION:
TELEPAX: (415) 398-3249
TELER: 910 27729
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                0.32;
                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Preu. ...
                                                        NAME: DUDI, TEACY D.
REGISTRATION NUMBER: 34,587
REFRENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-326-2402
INFORMATION FOR SEC 1D NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TVPPI: amino acids
TOPOLOGY: 11 near
APPLICATION NUMBER: US 07/740,375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08482728A Patent No. 5968802 GENERAL INFORMATION:
                  FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .LENGTH: 123 amino acids
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
These 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-142-897-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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STRANDEDNESS: unk
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APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: HONG, XIQIANG
APPLICANT: MA, DONG
TITLE OF INVENTION: NOVEL TYROSINE-CONTAINING
TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS
NUMBER OF SEQUENCES: 16
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83.7%; Score 41; DB 2; Length 123;

Query Match

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DB 2; Length 523;

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Patent No. 6150501

GENERAL INFORMATION:
APPLICANT: HONG, XIDIANG
APPLICANT: HONG, XIDIANG
TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS
INTURE OF INVENTION: CYCLOPHILIN AND RELATED METHODS
CORRESPONDENCE ADDRESS:
ADDRESSE: New England Biolabs, Inc.
STREET: STREET: STORE Road
CITY: Beverly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.6%; Score 40;
66.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOCTWARE: PRSESED VERSION 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEB-133
                                                      ATTORNEY CALL
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-
TELECOMMUNICATION INFORMATION:
TELEPAX: 978-927-5054
TELEFAX: 978-927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 978-927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 527 amino acids TYPE: amino acid
                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 978-927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                  APPLICATION NUMBER: FILING DATE:
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321 KFHRIIRNF 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KFHRVIKDF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 01915
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                                                                                                                                                                                                                                                                                                                                                                                                      US-09-028-366-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.7%; Score 41; DB 4; Length 523; 77.8%; Pred. No. 2.7; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NESULT BY SEQUENCE 2, APPLICATION US/09028366

Sequence 2, APPLICATION 105/09028366

PATENT NO. 6155501

APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: MA, DONG

TITLE OF INVENTION: NOVEL TYROSINE-CONTAINING

TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: New England Biolabs, Inc.

STREET: 32 Tozer Road
                                                                                                                                                                                                         OPERATIONS SYSTEM: DOS SOFTEMENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,366 FILLING DATE:
CLASSIFICATION NUMBER: US/09/028,366 FILLING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
APPLICATION NUMBER:
FILLING DATE:
NAME: WILLIAGE, GFGGOTY DESCRIPTION:
TELEFRONG/NOTION:
TELEFRONG/NOTION:
TELEFRONG: 978-927-5054
TELEFRONE: 978-927-5054
             E: New England Biolabs, Inc
32 Tozer Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FASTEM: DOS SOFTWARE: FASTEM VESTON 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/028,366 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                           COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 523 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 83.7
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1111:11:1
320 KFHRLIKNF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KFHRVIKDF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beverly
                                      STREET: 32 TO:
CITY: Beverly
                                                             CITY.
STATE: MA
COUNTRY: US
--- 01915
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Sequence 3, Application US/09134852;
Sequence 3, Application US/09134852;
Patent No. 6127148
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANYONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: DAVID G. CONLIN: DIKE, BRONSTEIN, ROBERTS &
ADDRESSE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STREET: USA
COUNTRY: USA
                                                                                                                    NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTY: UASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 176;
        APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 2
Pred. No. 2.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PRIOR PAPELICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.6%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 87.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||||||:|
64 FHRVIKNF 71
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US-09-134-852-3
                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
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                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MCHOD FOR IDENTIFYING ANTI-PARASITIC TITLE OF INVENTION: COMPOUNDS NUMBER OF SECURENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                     81.6%; Score 40; DB 4; Length 527; 66.7%; Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESMICK, DAVID S.
RECISTRATION NUMBER: 34235
REFERENCE/COCKET WUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAME (617) 523-6440
TELECAME (617) 523-640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-08-451-747-3
; Sequence 3, Application US/08451747
; Patent No. 5821107
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08145995A; Patent No. 5482850; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CARLOW, CLOTILDE K.S. APPLICANT: PAGE, ANTONY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS: single
unknown
                                                                                                                                                           Query Match 81.6
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-145-995A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
        ; STRANDEDNESS: single
; TOPOLGY: linear
; MOLECULE TYPE: protein
US-09-028-366-3
                                                                                                                                                                                                                                                                                          321 KFHRIIRNE 329
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Gaps

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Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                      Ouery Match 79.6%; Score 39; DB 4; Length 269; Best Local Similarity 87.5%; Pred. No. 3.4; Matches 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 1; Length 591; Pred. No. 7.2; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IN TOTAL AND TO COMPATION COMPUTER: IN PC COMPATION NUMBER: US/08/145,995A FILING DATE: 29-OCT-1993 CLASSIFICATION: 435 ATTONEY MACHATION: WANES: RESULCE, DAVID S. REGISTRATION NUMBER: 34235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/08145995A
Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
                                                                     INFORMATION FOR SEQ 1D NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 269 amino acids: TYPE: amino acid STRANDEDNESS: single STRANDEDNESS: single MOLECULE TYPE: protein US-09-028-366-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 43
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.68;
87.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 591 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 87.35
7: Conservative
                                      TELEFAX: 978-927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-145-995A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 FHRVIKDF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-145-995A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: HONG, XIQIANG
APPLICANT: HONG, XIQIANG
TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: New England Biolabs, Inc.
STREET: Beverly
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/134,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB :
Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                      FILING DATE:
CLASSPECATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/145,995
FILICATION NUMBER: US 08/145,995
ATTORNEY AGENT INFORMATION:
NAME: RESINCK, DAVID S.
REGISTARTION NUMBER: 34.35
REFERENCE/DOCKET NUMBER: 43406
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECAX: (617) 523-6440
TELEFAX: (617) 523-6440
TELEFAX: (617) 523-6440
TELEFAX: (700291 STRE UR
TELEFAX: (700291 STRE UR
TELEFAX: (700291 STRE UR
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PSASEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION UNMBER: 30901
REFERENCE/POCKET NUMBER: NEB-133
TELECOMUNICATION INFORMATION:
TELEPHONE: 978-927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09028366
Patent No. 6150501
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 87.55
Tr Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAtibl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-134-852-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FHRVIKDF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Beve
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-028-366-6
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RESULT 15
US-08-451-747-21
Sequence 21, Application US/08451747
Sequence 21, Application US/08451747
Sequence 21, Application US/08451747
Sequence 21, Application US/08451747
GEMERAL INFORMATION:
APPLICANT: PAGE, ANTONT
TITLE OF INVENTION: WETHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES:
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC:
STREET: 32 TOZER ROAD
CITY: BEVERLY
STREET: AMSSACHUSETTS
COUNTRY: USA
ZIP: 01915
COMPUTER: TIM PC COMPATIBLE
COMPUTER: TIM PC COMPATIBLE
COMPUTER: TAM PC COMPATIBLE
SOFTWARE: PATENTIN BYTHE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
FILLING DATE:
CLASSIFOTOMER:
CLASSIFOTOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTATION UNMBER: 30901
REFERENCE/DOCKET NUMBER: 30901
REFERENCE/TOCKET NUMBER: 08901
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-451-747-21
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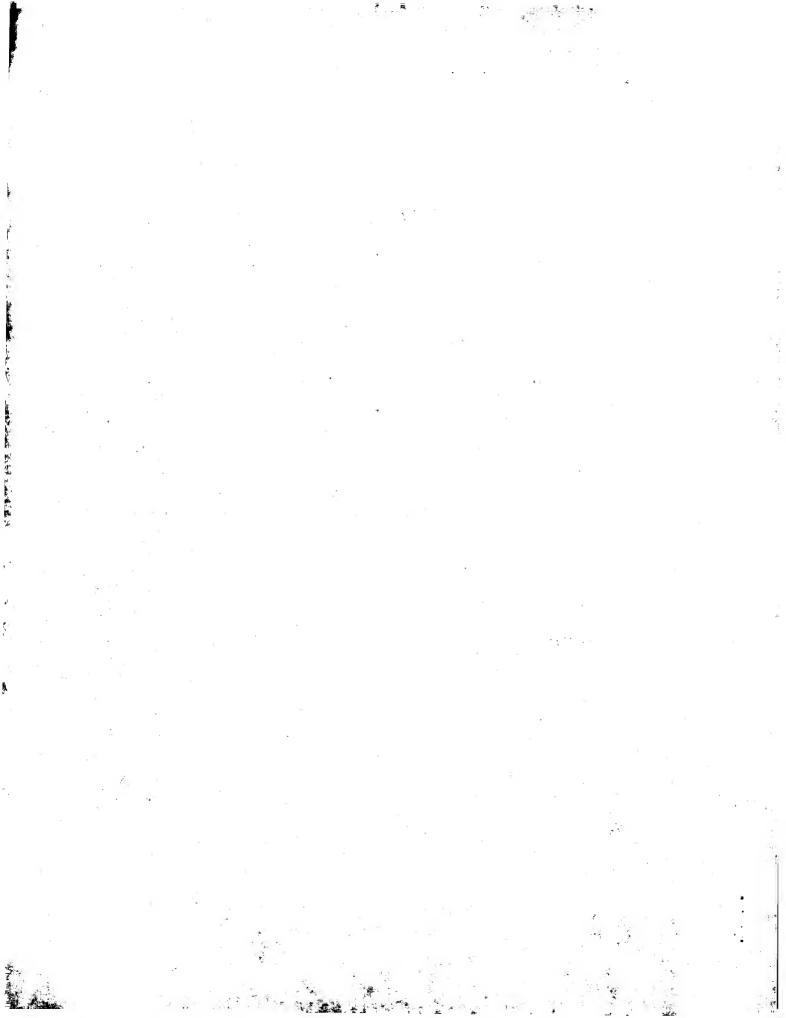
; Query Match 79.6%; Score 39; DB 2; Length 591; Best Local Similarity 87.5%; Pred. No. 7.2; Matches 7; Conservative 1; Mismatches 0; Indels

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2 FHRVIKDF 9 ó

q

Search completed: January 15, 2002, 13:03:58 Job time: 214 sec



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; Search time 42.04 Seconds
(without alignments)
16.308 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                        January 15, 2002, 13:02:29
                                                                                         OM protein – protein search, using sw model
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US-09-720-469-1 KFHRVIKDF 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9 100.0 183 2 571547 Peptidylprolyl 100.0 207 2 A40516 Peptidylprolyl 100.0 208 267 2 A54204 Peptidylprolyl 100.0 216 2 A56861 Peptidylprolyl 100.0 216 2 A56861 Peptidylprolyl 100.0 216 2 A71261 Peptidylprolyl 100.0 216 2 A71261 Peptidylprolyl 100.0 2 7212 2 72120 Peptidylprolyl 100.0 2 72120 Peptid	Scor	1	ry l		DB	ID.	Description
9 100.0 207 2 A40516 peptidylprolyj 100.0 208 1 C8HUB peptidylprolyj 100.0 216 2 A56861 peptidylprolyj 2 F84808 peptidylprolyj 2 F84808 peptidylprolyj 100.0 216 2 A40047 peptidylprolyj 2 A500 2 B53422 peptidylprolyj 2 A500 2 B5332 peptidylprolyj 2 A500 2 B5333 peptidylprolyj 2 A500 2 B5333 peptidylprolyj 2 A500 2 B53423 peptidylprolyj 2 A500 2 A500 2 B500 2	4		0.	183	ď	S71547	_
9 100.0 208 1 CSHUB 9 100.0 212 2 A54204 9 100.0 212 2 A54204 9 100.0 212 2 A54801 100.0 216 2 A54801 100.0 216 2 E84808 100.0 216 2 E84808 100.0 216 2 A40047 100.0 215 2 A40047 Pertidylprolyl 2 E85867 100.0 216 2 E86736 1	4		0.	207	7	A40516	
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4 89.8 215 2 771261 peptidylprolyl 89.8 371 2 848567 cyclophillin-lik 87.8 204 2 F21587 peptidylprolyl 87.8 204 2 F21587 peptidylprolyl 87.8 264 2 G2477 peptidylprolyl 87.8 754 1 JC5314 CCC28/cdc2-like 2 G8777 peptidylprolyl 87.7 57.8 2 C8777 probable 40 kd 87.7 57.8 2 C73003 peptidylprolyl 87.6 12 C7303 peptidylprolyl 87.6 155 2 F38930 peptidylprolyl peptidylprolyl 87.6 155 2 F38930 peptidylprolyl Peptidylprolyl 77.6 155 2 F38930 peptidylprolyl 87.6 172 2 F37890 peptidylprolyl 87.6 172 2 F37890 peptidylprolyl 77.6 172 2 F37890 peptidylprolyl 87.6 172 2 F37890 peptidylprolyl 77.6 192 2 F37890 peptidylprolyl 77.6 193 2 F	4	~	<b>&amp;</b>	212	~	A40047	
4 89.8 371 2 548567 Cyclophilin-lik 89.8 136 2 886736 Peptidylprolyl 87.8 260 2 85342 Peptidylprolyl 13 87.8 260 2 85342 Peptidylprolyl 13 87.8 260 2 85342 Peptidylprolyl 14 12 85.7 164 1 265314 Cyclophilin-lik 98.7 523 2 56237 Peptidylprolyl 18 3.7 523 2 56237 Peptidylprolyl 18 3.7 523 2 56237 Peptidylprolyl 18 3.7 523 2 56327 Peptidylprolyl 19 75.6 140 2 84633 Peptidylprolyl 19 77.6 152 2 738930 Peptidylprolyl 17 6 152 2 52802 Peptidylprolyl 17 6 162 1 5 5 2 73880 Peptidylprolyl 17 6 17 2 574880 Peptidylprolyl 17 6 17 2 177371 Peptidylprolyl 17 6 17 6 17 6 17 6 17 6 17 6 17 6 17	4	4	89.	215	7	A71261	peptidylprolyl iso
43 87.8 196 2 E86736 peptidyl-prolyl 43 87.8 260 2 E86736 peptidyl-prolyl 43 87.8 260 2 E853422 peptidylprolyl 43 87.8 754 1 JC5314 CDC28/CdC2-like 42 85.7 164 2 CS2314 CDC28/CdC2-like 41 83.7 356 2 S6237 peptidylprolyl 41 83.7 523 2 T23003 peptidyl-prolyl 57.6 410 2 E8433 peptidylprolyl 57.6 141 2 E86934 peptidylprolyl 57.6 155 2 T38930 peptidylprolyl 57.6 162 1 CS87 peptidylprolyl 57.6 162 1 CS87 peptidylprolyl 57.6 162 2 S28020 peptidylprolyl 57.6 172 2 T2383 peptidylprolyl 57.6 172 2 T2383 peptidylprolyl 58 77.6 172 2 T27831 peptidylprolyl 77.6 172 2	4	4	89.	371	~	548567	cvclophilin-like n
3 87.8 204 2 721587 Peptidylprolyl 3 87.8 260 2 853422 Peptidylprolyl 3 87.8 754 1 JC5314 CDC28/cdc2-ixel 2 85.7 164 2 C8477 CDC28/cdc2-ixel 2 85.7 164 2 C8477 CDC28/cdc2-ixel 2 83.7 356 2 853327 Probable 40 kd 81.6 201 2 T18573 Peptidylprolyl 1 Peptidylprolyl 2 77.6 155 2 T38930 Peptidylprolyl 2 77.6 155 2 T38930 Peptidylprolyl 2 77.6 155 2 T38930 Peptidylprolyl 2 77.6 152 1 CSBY Peptidylprolyl 2 77.6 171 2 T27880 Peptidylprolyl 2 77.6 171 2 T27880 Peptidylprolyl 2 77.6 171 2 T27880 Peptidylprolyl 2 77.6 172 2 T27880 Peptidylprolyl 2 77.6 172 2 T27880 Peptidylprolyl 2 77.6 172 2 T27881 Peptidylprolyl 2 77.6 173 2 T27881 Peptidylprolyl 1 77.6 173 2 T27881 Peptidylprolyl 1 77.6 173 2 T27881 Peptidylprolyl 1 77.6 192 2 T27881 Peptidylprolyl 1 77.6 192 2 T27882 Peptidylprolyl 1 77.6 192 2 T27883 Peptidylprolyl 1 77.6 193 2 T27883 Peptidylprolyl 1 77.6 193 2 T27883 Peptidylprolyl 1 77.6 193 2 S7050 Peptidylprolyl 1 77.6 193 2 S7050	4	3	ω.	196	~	E86736	nentidal-nrolal ci
3         87.8         260         2         B53422         Peptidylerolyl           3         87.8         754         1         C5314         C62457         C62457         C62457         C62457         C624626-11ke           1         83.7         552         2         S6237         C7010philin         C7010p	4		80.	204	7	T21587	pentidylprolyliso
3 87.8 754 1 JC5314 CDC28/cdc2-1/ke 2 85.7 164 2 C84777 Cyclophilin-lik 1 83.7 553 2 T23003 Probable 40 kd 1 83.7 5 12 2 H8573 Probable 40 kd 1 77.6 141 2 H69044 Probable 40 kd 1 77.6 155 2 T38930 Probable 40 kd 1 77.6 165 2 S28020 Probable 40 kd 1 77.6 171 2 S74880 Probable 40 kd 1 77.6 171 2 T27871 Probable 40 kd 1 77.6 172 2 T27881 Probable 40 kd 1 77.6 172 2 T27882 Probable 40 kd	4		ω.	260	~	B53422	peptidylprolyliso
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183.7 356 2 562327   Probable 40 kd     183.7 523 2 72303   Probable 40 kd     183.7 523 2 72303   Probable 40 kd     183.7 523 2 72303   Propertical propertica	7		۲.	164	~	C84777	cyclophilin-like p
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0 81.6 201 2 718573 peptidylprolyl 9 79.6 404 2 D84533 hypothetical pr 77.6 141 2 H69044 peptidylprolyl 8 77.6 152 1 CSBY peptidylprolyl 77.6 162 1 CSBY peptidylprolyl 8 77.6 171 2 57480 peptidylprolyl 8 77.6 171 2 172371 peptidylprolyl 8 77.6 172 2 T2783 peptidylprolyl 8 77.6 172 2 T2783 peptidylprolyl 8 77.6 172 2 T2783 peptidylprolyl 8 77.6 192 2 T2783 peptidylprolyl 8 77.6 192 2 T2783 peptidylprolyl 8 77.6 393 2 S57050 CCClobilininily	4	_	۲.	523	7	T23003	٠,
9 79.6 404 2 D84533 hypothetical pr 8 77.6 141 2 H69044 peptidylprolyl 8 77.6 162 1 CSBY peptidylprolyl 8 77.6 162 2 S28020 peptidylprolyl 8 77.6 171 2 S74880 peptidylprolyl 8 77.6 171 2 T27371 peptidylprolyl 8 77.6 172 2 T27832 peptidylprolyl 8 77.6 172 2 T27832 peptidylprolyl 8 77.6 172 2 T27834 peptidylprolyl 8 77.6 172 2 T27034 peptidylprolyl 8 77.6 393 2 S57050 ccclobilinilinily	4	0	9	201	~	T18573	
17.6   141   2   H69044   Peptidylprolyj   17.6   155   2   138930   Peptidylprolyj   17.6   165   2   228020   Peptidylprolyj   Peptidylprolyj   17.6   165   2   228020   Peptidylprolyj   17.6   171   2   27371   Peptidylprolyj   Peptidylprolyj   17.6   172   2   127831   Peptidylprolyj   17.6   172   2   127832   Peptidylprolyj   17.6   192   2   127034   Peptidylprolyj   17.6   192   2   127034   Peptidylprolyj   17.6   393   2   257050   Carolophilianianianianianianianianianianianianiani	е	o	9.	404	N	D84533	14
77.6   155   2   138930   Peptidylprolyl   17.6   162   1   1281   Peptidylprolyl   17.6   162   1   1281   Peptidylprolyl   17.6   17.1   2   127371   Peptidylprolyl   17.6   17.2   17.3   17.8   17.6   17.2   17.3   Peptidylprolyl   17.6   17.2   17.3   17.6   17.3   17.0   17.3   Peptidylprolyl   17.6   17.2   17.3	m	æ	ب	141	7	H59044	
17.6   162   CSBY   Peptidylprolyl   Petidylprolyl   Pe	m	œ	9.	155	~	T38930	
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8 77.6 171 2 127371 Peptidylprolyl 8 77.6 172 2 127882 peptidylprolyl 8 77.6 172 2 1706073 peptidylprolyl 8 77.6 192 2 127034 peptidylprolyl 8 77.6 393 2 557050 cvclophilianlika	m	<b>&amp;</b>	9.	171	7	\$74880	
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probable cyclophil hypothetical prote	natural killer cel natural killer cel	TMV resistance pro Ran-binding protei	peptidylprolyl iso peptidylprolyl iso	1	7.7.	idylprolyl i	
T41399 T27467	A47328 B47328	T04583 S58884	T18577 F81156	T29283 T27373	A53522 JT0686	S30507 T18575	<b>T49181</b> <b>A84</b> 611
22	7	7 7	00	77	77	~ ~	0.0
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77.6	77.6	77.6	75.5	75.5	75.5	75.5	75.5
388	ထထ	20 20 20 20 20 20	37	37	37	37	37
30	33.2	ლო: •	36 37	ස <b>ර</b> ෆ ෆ	<b>7 7</b> 0	4 4 2 2	44 5

## ALIGNMENTS

Gaps 0; 100.0%; Score 49; DB 2; Length 183; larity 100.0%; Pred. No. 0.021; Conservative 0; Mismatches 0; Indels Ouery Match Best Local Similarity

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0;

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A40516

Peptidylprolyl isomerase (EC 5.2.1.8) (S-cyclophilin) precursor - chicken Cispecies: Gallus Gallus (chicken)
Cispecies: Gallus Gallus (chicken)
Cispecies: Gallus Gallus (chicken)
Cistesion: A40516
Ricaroni, P. 1, Rothenfluh, A.; McGlupu, E.; Schneider, C.
A; File: S-cyclophilin. New member of the cyclophilin family associated with the secr A; Feference number: A40516; MuID:91250364
A; File: S-cyclophilin. New member of the cyclophilin family associated with the secr A; Reference number: A40516
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-207 < CARA
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C; Meywords: cistrans-isomerase; cyclosporin A binding
F; 34-196/Domain: cyclophilin homology <CYP>

Gaps ó Ouery Match
100.0%; Score 49; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels

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A:Rolecule type: mRNA
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A:Residues: 1-216 <SCH
A:Residues: 1-216 <SC
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C;Comment: This protion is distinguished from peptidylprolyl isomerase A by the prese
C;Soperfamily: peptidylprolyl isomerase: cyclophilin homology
C;Keywords: cis:trans-isomerase; cyclosporin A binding; endoplasmic reticulum; T-cell
F;1-33/Domain: signal sequence #status predicted <SIG>
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NAlternate names: cyclophilin B; cyclophilin-SI; cyclosporin A-binding protein
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Aus musculus (house mouse)
C;Accession: A56861; B39722; S21835
R;Schumacher, A.; Schroter, H.; Multhaup, G.; Nordhelm, A.
Biochim: Biophys. Acta 1129, 13-22, 1991
A;Title: Murine cyclophilin-SI: a variant peptidyl-prolyl isomerase with a putative s
A;Reference number: A56861; MulD:92096454
                                                                                                                                                                                                                             R;Schneider, H.; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zurlni, M.G.; Quesn Biochemistry 33, 8218-8224, 1994
A;Title: Human cyclophilin C: primary structure, tissue distribution, and determination, A;Reference number: A54204; MUID:94304830
                                                                                              C;Species: Homo sapiens (man)
C;Date: 22-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: kidney
A; Note: sequence extracted from NCBI backbone (NCBIN:149387, NCBIP:149388)
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A;Residues: 1-212 <SCH>
A;Cross-references: GB:S71018; NID:g547303; PIDN:AAB31350.1; PID:g547304
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C:Superfamily: peptidyprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding
F;37-199/Domain: cyclophilin homology <CYP>
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peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human
N;Alternate names: cyclophilin C
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100.0%; Pred. No.
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A;Reference number: $21835
A;Accession: $21835
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Best Local Similarity 100.
Matches 9; Conservative
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A; Residues: 9-216 <NOR>
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A; Residues: 9-216 <HAS>
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                                                                                                                                                                                                                                                                                                                           Ushub peptidylprolyi isomerase (EC 5.2.1.8) B precursor [validated] - human NyAlternate names: cyclophilin B: cyclosporin A-binding protein B: S-cyclophilin C; Species: Homo sapiens (man)
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Dec-2000
C; Date: 31-Mar-1992 #sequence_revision Mar-1992 #text_change 08-Dec-2000
A; Title: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl isomer A; Restdues: 1-208 cPRI>
A; Residues: 1-208 cPRI>
A; Cossion: A39118
A; Cossion: A3912; MUD:9181334; PIDN:AAA52150.1; PID:9181335
B; Hasel, K. W.; Glass, J. R.; Godbout, M.; Sutcliffe, J.G.
A; Title: An endoplasmic reticulum-specific cyclophilin.
A; Reference number: A39722; MUD:91260697
A; Accession: A39722; MUD:91260697
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A;Titler: Evidence that human milk isolated cyclophilin B corresponds to a truncated form A; Reference number: S65742; MUID:96186273
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein a Relaction is distinguished from peptidylprolyl isomerase A by the presence C;Comment: This protein is distinguished from peptidylprolyl isomerase A by the presence C;Comment: This protein binds to and is inhibited by the immunosuppressive drug cyclospe
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A; Rosaldus: 1-208 (4-M5>
A; Rosaldus: 1-208 (4-M5>
A; Cross-references: GB: M60457; NID:g181249; PIDN: AAA35733.1; PID:g181250
B; Splk, G.; Haendler, B.; Delmas, O.; Mariller, C.; Chamoux, M.; Maes, P.; Tartar, A.; J. Balol. Chem. 266, 10735-10738, 1991
A; Ttle: A novel secreted cyclophilin-like protein (SCYLP).
A; Reference number: A40515; MUID:91250363
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A)Cross-references: GDB:127610; OMIM:123841
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C; Function:
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C;Accession: A40047
R;Friedman, J.; Weissman, I.
Cell 66, 799-806, 1991
A;Title: Two cytoplasmic candidates for immunophilin action are revealed by affinity A;Reference number: A40047: MUID:91347379
A;Accession: A40047
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C:Species: Trepomem pallidum subsp. pallidum (syphilis spirochete)
C:Species: 24.Jul-1998 #sequence_revision 24.Jul-1998 #text_change 08.Sep-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptidylprolyl isomerase (EC 5.2.1.8) (cyclophilin C) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 *sequence_revision 30-Jun-1992 *text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                     Gaps
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           A:Introns: 34/3; 87/3; 148/1
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:16-183/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                 Indels
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0.24;
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. 0.24;
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0.21;
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0; Mismatches
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                                                                                                                                                                                                                      89.8%; Score 44; 100.0%; Pred. No.
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                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.(
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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A; Residues: 1-212 <FRI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                  71 FHRVIKDF 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 FHRVIKDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable peptidyl-prolyl cis-trans isomerase [imported] - Arabidopsis thaliana (Grander et al., 2001) | Crander et al., 2001 | Crander et
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C;Accession: T18578; T24269
R;Page, A.P.; MacNiven, K.
submitted to the EMBL Data Library, August 1995
                                                                                                                                                                                                                      Gaps
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F:34-216/Product: peptidylprolyl isomerase B #status predicted <MAT>F:43-205/Domain: cyclophilin homology <CYP>
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                                                                                                                                               Length 216;
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C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
                                                                                                                                               DB 2;
                                                                                                                                           100.0%; Score 49; DB 2; 100.0%; Pred. No. 0.025;
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A;Residues: 1-183 <PAG>
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Subarter to the EMBL Data Library, October 1995
A;Afference number: 219867
A;Accession: T24269
                                                                                                                                                                                                               0; Mismatches
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A;Experimental source: strain Bristol N2
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                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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A;Accession: T18578
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A;Molecule type: DNA
A;Residues: 1-199 <STO>
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Peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thallane
Nylternate names: cyclophill, homolog ROC4; protein F21F14.200
C;Species: Arabidopsis thallana (mouse-ear cress)
C;Date: 19-May-1995 #sequence_revision 19-Nay-1995 #text_change 19-May-2000
C;Accession: B53422; T47995
J. Biol. Chem. 269, 7863-7868, 1994
A;Ttle: Cloning and characterization of chloroplast and cytosolic forms of cyclophil A;Reference number: A53422; MUID:94179146
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A;Residues: 1-260 <LLIP>
A;Cross-references: GB:L14845; NID:g405130; PIDN:AAA20048.1; PID:g405131
R:Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.;
submitted to the Protein Sequence Database, February 2000
                                                                                                                                                                                                                                                          peptidylprolyl isomerase (EC 5.2.1.8) F31C3.1 [similarity] - Caenorhabditis elegans
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A;Experimental source: clone F31C3
                                                                                                                                                                                                                                                                                                   N.Contains: cyclophilin
C.Species: Caenorhabditis elegans
C.Date: 15-00t-1999 #sequence_revision 15-0ct-1999 #text_change 02-Sep-2000
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C;Keywords: cis-trans-isomerase
F;28-190/Domain: cyclophilin homology <CYP>
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A;Residues: 1-260 <CHO>
A;Cress references: EMBL:AL]38642
A;Experimental source: cultivar Columbia: BAC clone F21F14
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A;Nolecule type: DNA
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88.9%; Pred. No. 0.36;
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A;Introns: 18/3; 81/3; 133/1; 162/3; 181/1; 209/3
A;Note: F21F14.200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Cottage, A.
submitted to the EMBL Data Library, March 1997
A;Reference number: 219446
A;Accession: Y21887
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Best Local Similarity
Matches 8; Conserv
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A;Gene: CESP:F31C3,1
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2 FHRVIKDF
                                                                     55 FHRIIKDF
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A; Introns: 69/3
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E86736
peptidyl-prolyl cis-trans isomerase [imported] - Lactococcus lactis subsp. lactis (strai c. Species: Lactococcus lactis subsp. lactis
C. Species: Lactococcus lactis subsp. lactis
C. Species: Lactococcus lactis subsp. lactis
C. Accession: E86736
R. Boloctin, A.: Wincker, P.: Mauger, S.: Jaillon, O.: Malarme, K.: Weissenbach, J.: Ehrli
Genome Res. in press, 2001
A.:Title: The complete genome sequence of the lactic acid bacterium.
A.:Reference number: A86625
A.:Accession: E86736
A.:Accession: E86736
A.:Accession: E86736
A.:Molccule type: DNA
A.:Experimental source: strain IL1403
C.:Genetics:
A.:Genetics:
A.:Gen
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A. Residues: 1-371 cPAU>
A. Cross-references: EMBL:U14913; NID:9544497; PIDN:AAB67445.1; PID:9544520; MIPS:YLR216c
A. Cross-references: EMBL:U14913; N. R. F.
Yeast 12, 943-952, 1996
A.711Lie: Identification of two CyP-40-like cyclophilins in Saccharomyces cerevisiae, one
A. Reference number: S71742; MUID:97027304
A. Reference number: S71742
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C; Genetics:
                                                                                                                                                                                                                                                                                               Gyclophilin-like protein CPR6 - yeast (Saccharomyces cerevisiae)

(Nathernate names: protein L8167.24; protein YLR216c

(Sychaes: Saccharomyces cerevisiae

(Species: Saccharomyces)

(Species: Saccharomyces

(Species: Salb567; S71742

(Species: Salb567; S71742

(Species: Salb567; S71742

(Species: Salb567; S71742

(Species: Salb567)

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(Species: Salb567)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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100.0%; Pred. No. 0.43;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: SGD:CPR6; CYP40
A;Cross-references: SGD:S0004206; MIPS:YLR216c
A;Map position: 12R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 89.8
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-371 <DUI>
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62 FHRVIKDF 69
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                                         2 FHRVIKDF
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DB 2; Length 260;

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Search completed: January 15, 2002, 13:06:15
Job time: 226 sec
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A; Residues: 1-754 <NES>
A; Residues: 1-754 <NES>
A; Cross-references: EMBL:040763; NID:g1117967; PIDN:AAB40347.1; PID:g1117968
A; Experimental source: thymus
A; Experimental source: thymus
A; Kote: submitted to the EMBL Data Library, November 1995
C; Comment: This protein contains a cyclophilin-related domain, two 140K nuclear phosphop splicing by binding to splicing factors containing serine-arginine repeats protein.
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Cyclophilin-like protein [imported] - Arabidopsis thaliana
Cispectas: Arabidopsis thaliana (mouse-ear cress)
Cispectas: Arabidopsis thaliana (mouse-ear cress)
Cispectas: Arabidopsis thaliana (mouse-ear cress)
Cispectas: C84777
Rilin, X.: Kaul, S.: Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.: Koo, H.: Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.: Nierman, W.C.; White, O.: Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487 A;Accession: C84777 A;Status: preliminary
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A;Residues: 1-164 <STO>
A;Cross-references: GB:AE002093; NID:94678225; PIDN:AAD26970.1; GSFDB:GN00139
                                                                                                                                                                                                                                                                                                   UC5314

UCC28/cdc2-like kinase associating arginine-serine cyclophilin - human
N.Alternate names: CARS-Cyp
N.Alternate names: CARS-Cyp
C; Species: Homo sapiens (man)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
R; Nestel, F.P.: Colvail, K.; Harper, S.; Pawson, T.; Anderson, S.K.
Gene 180, 151-155, 1996
A:Title: RS cyclophilins: Identification of an NK-TR1-related cyclophilin,
A:Title: The cyclophilins is identification of an NK-TR1-related cyclophilin,
A:Title: The cyclophilins is identification of an NK-TR1-related cyclophilin,
                                                                       Gaps
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Pred. No. 1.4;
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Pred. No. 0.46;
2; Mismatches 0; Indels
                                                                    0; Indels
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C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A: Cross-references: GDB:9956062
C:Superfamily: CARS cyclophilin; cyclophilin homology
F;7-177/Domain: cyclophilin homology <CYP>
                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
   87.5%; Score 43;
87.5%; Pred. No. (
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 87.5
Query Match 87.8
Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                144 FHRIIKDF 151
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65 FHRVVKDF 72
                                                                                                                        2 FHRVIKDF 9
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us-09-720-469-1.rsp

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 15, 2002, 13:04:04; Search time 24:88 Seconds (without alignments) 13:263 Million cell updates/sec Run on:

US-09-720-469-1 49 1 KFHRVIKDF 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	367 qa	1 bos tau	homod	m snm 6	7 homo	8 caeno	~	O66105 treponema p	1 saccharom	P52013 caenorhabdi	P34791 arabidopsis	8	P52012 caenorhabdi	P52014 caenorhabdi	_		P14832 saccharomyc	000060 uromyces fa	Q06118 streptomyce	Ö	P52015 caenorhabdi	P34790 arabidopsis	P52009 caenorhabdi	P47103 saccharomyc	P48820 bos taurus	P30415 mus musculu	4 homo	2 homo	7 caenc		P25719 saccharomyc	P52016 caenorhabdi	_
SUMMARIES		ΩI	CYPB_CHICK	CYPB_BOVIN	CYPB_HUMAN	CYPB_MOUSE	CYPC_HUMAN	CYPB_CAEEL	CYPC_MOUSE	PPIB_TREPA	CYP6_YEAST	CYP5_CAEEL	CYP4_ARATH	CYPB_RAT	CYP4_CAEEL	CYP6_CAEEL	CYP1_BRUMA	CYP2_SCHPO	CYPH_YEAST	CYPH_UROFA	PPI_STRCH	CYP2_CAEEL	CYP7_CAEEL	CYP1_ARATH	CYP1_CAEEL	CYP7_YEAST	RBP2_BOVIN	NKCR_MOUSE	NKCR_HUMAN	RBP2_HUMAN	CYPA_CAEEL	CYP3_CAEEL	CYPC_YEAST		CYP9_CAFEL
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of	Query	Match	100.0	100.0	100.0	100.0			8.68	86.8	8.0	87.8	87.8	~	83.7	81.6	79.6	77.6	77.6	77.6	77.6		77.6	77.6	٠	9'/	٠	17.6	77.6		'n.	75.5	ď.	S.	73.5
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Gaps

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Query Match
100.0%; Score 49; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels

NN P26882 bos taurus O08752 homo sapien P14088 echinococcu P54985 blattella g O9ye67 aeropyrum p P21569 zea mays (m O9y33 drosophila O9y33 drosophila P05374 saccharomyc P2507 drosophila O49886 lupinus lut D71578 mycobacterica P42693 acinetobact	IENTS	207 AA.	update) n update) B PRECURSOR (EC 5.2.1.8) (PPIASE) HILIN) (SCYLP).	a; Vertebrata; Euteleostomi; ormes; Phasianidae; Phasianinae;		E., Schneider C.; cyclophilin family associated with	SECTECTY PAIRWAY."  SECTION: 266:10739-10742(1991).  FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.  CATALITIC CATALITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC	SITS CYPB. LUMEN (BY SIMILARITY PPIASE FAMILY.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/	(n.)	Signal: Endoplasmic reticulum:	YL CIS-TRANS	Y SIMILARITY). D9CGCZE528RZ5B59 CRC64;
CYP4_BOVIN CYP4_HUMAN CYP4_ECHGR CYP4_BLAGE TP6A_AERPE CYP4_MAIZE CYP4_BROME PEM1_YEAST CYP4_DROME CYP4_LUPLU PPIA_MYCTU	ALIGNMENT	PRT;	ted) sequence update annotation upda ISOMERASE B PREC (S-CYCLOPHILIN)	Craniata; Ver Galliformes;		93; Ynn E., the cyc	(1991). TE THE	ORIN A PLASMIC CYCLOF	yright. I of Bioir Institute tions as is not re	D-S1D.C	و با جا جا جا	BY SIMILARITY PEPTIDYL-PROL PREVENT SECRE	D9COCZ
P P C C C C C C C C C C C C C C C C C C			ted se an ISO			Pubmed-2040593 luh A., McGlyn w member of th	10742 ELERA IS-TR	CLOSP ENDO THE	copyr ute o cs In ituti nt is	Sed15	9064.1; 1. 1. 1. CSA PPIASE. 1. SAPPISSE. 1. SAPPISMRASE. CSA_PPIASE. 1. CSA_PPIASE. 2. 2. 2. 2. 2. 2. 3. 3. 3. 4. 5. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6.	യാഹഹ	MW;
370 370 161 161 172 385 390 172 182 182		RD;	Creat Last Last RANS ]	ken). Chordata; Neognathae		Med- A., embe	739-	CY( CY( ION:	try is col Instituti formatics it institut statement	cen	f.l; CSA_I Omera PISMi PPI/	477	413
ммппмпммннн		STANDARD;	21, 21, 38, IS-T PHIL	(Chicken) azoa; Cho ves; Neog		Publ fluh ew m	6:10 ASES IVIT	TION	ntry s Inv nfor it sta	01	49064. 116. 30; CS 30; CS 52. CSAPPI CSA_P CSA_P	000	; 22
733.55 6699.44 77.11.55 77.11.669 73.44 74.667 75.73 76.73		ST	Rel. Rel. YL C	tazo Aves	31;	N.A. 364; othenf n. Ne	PPI PPI PPI	GULA GULA AR L	ROT entress In Bioinfo	. 11 Bi	AAA A405 1CY 00021 0, Pr 170; 170; 150; 150;	family. 1 25 2 198 2	7 AA
<b>νουνυ444</b> ωωωω		×	992 (992 (999 (	a; Me	)6 <b>=</b> 0:	FROM 12500 Rot Phillic	Chem	TE REST	SS-PF the ron non- and requ	in em	1553; 1284; 1284; 1284; 1286; 1286; 1286;		207
wwwwwwwwww	-	T 1 CHICK CYPB_CHICK P24367:	01-MAR-1992 (Rel. 21, Crea 001-MAR-1992 (Rel. 21, Last 15-JUL-1999 (Rel. 38, Last PEPTIDYL-PROLYL CIS-TRANS (ROTAMASE) (CYCLOPHILIN B)	Gallus gallus (Chicken). Eukaryota, Metazoa, Chordata, Archosauria, Aves, Neognathae Gallus.	NCBI_TaxID=9031	===	ne secre . Biol. !- FUNCT !- CATAI		This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinfo the European Bioinformatics Institute. Would by non-profit institutions as low modified and this statement is not remoentities requires a license agreement (	send a	EMBL, M65553, AAA49064.1; PIR: A40516; A40516. HSSP: P23284; ICVN. InterPro; IPR002130; CSA_PPIase Pfam; PF00160; pro_isomerase; I PRINTS; PR00153; CSA_PPISMASE_I); PROSITE; PS00170; CSA_PPIASE_I; PROSITE; PS00772; CSA_PPIASE_I; CVCLOSPORTIN; ISOMERASE.	Multigene SIGNAL CHAIN SITE	SEQUENCE
88888888888888888888888888888888888888		ESULT YPB_CH D CY	15 15 7 8	G A E	NCB [1]	R E S S	5,77		L Charles Charles	5 : 2	PP	MU SI CH SI	S
	000	RESUL CYPB_ ID	01 01 02 03	8888	O R	RAK	4 4 8 8 8 E	38888	38888888	388	70000XXX	X F F F F	SO

Pred. No. 0.015;

100.0%;

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Best Local Similarity
Matches 9; Conserv
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P23284;
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CYPB_HUMAN
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                                                                                                                                                                                                                                                                                  01-0UN-1994 (Rel. 29, Created)
01-NUN-1995 (Rel. 32, Last sequence update)
12-UL-1999 (Rel. 38, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Galat A., Bouet F.;
'cyclophilin-B is an abundant protein whose conformation is similar
to cyclophilin-A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             œ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Netazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PREVENT SECRETION FROM ER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bose S., Muccke M., Freedman R.B.; "The characterization of a cyclophilin-type peptidyl prolyl cis-trans-isomerase from the endoplasmic-reticulum lumen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carrello A., Mark P.J., House A.K., Ratajczak T.;
Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
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0097C88289AF6276 CRC64;
                                                                                                                                                                                                                                 208 AA.
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Pfam: PF00160; pro_isomerase: 1.
PRINTS: PR00153; CSAPPISMRASE.
PR051TE; PS00170; CSA_PPIASE_1: 1.
PR05ITE; PS50072; CSA_PPIASE_2: 1.
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22701 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                taurus (Bovine).
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                                 1 KFHRVIKDF
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01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1991 (Rel. 20, Last sequence update)
PEPPIDYL-PROLYL CIS-TRANS ISOMERASE B PRECHRSOR (EC 5.2.1.8) (PPIASE)
(ROMAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl isomerase with a signal sequence.";
Proc. Natl, Acad. Sci. U.S.A. 88:1903-1907(1991).
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-!- FUNCTION: PPIASES ACCELERATE THE POLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mikol V., Kallen J., Walkinshaw M.D.;
M.Y.ray structure of a cyclophilin B/cyclosporin complex: compa
with cyclophilin A and delineation of its calcineurin-binding
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 26-40.
MEDLINE-91156714; PubMed-2000394;
Price E.R., Zydowsky L.D., Jin M., Hunter C.H., McKeon F.D.,
Walsh C.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92112948; PubMed=1530944; Arber S., Krause K.-H., Caronl P.; S-cyclophilin is retained intracellularly via a unique CC sequence and colocalizes with the calcium storage protein calreticulin.";
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    Indels
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                                                                                                                                                                    208 AA.
    Mismatches
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MEDLINE=93162043; Pubmed=1286667;
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    Conservative
                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                        84 KFHRVIKDF 92
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                                          1 KFHRVIKDE
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SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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PIR; S21835; S21835.
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MGD; MGI:97750; Ppi
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Matches 9; Conser
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01-WAR-1992 (Rel. 21, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PEPTIONL-PROMYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY
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MEDLINE-91260697; Pubmed-1710767;
MEDLINE-91260697; Pubmed-1710767;
MEDLINE-91260697; MISHAGE J.R., Godbout M., Sutcliffe J.G.;
"An endoplasmic reticulum specific cyclophilin.";
Mol. Cell. Biol. 11:3484-3491(1991).
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EMBL: M60457; AAA35733.1; -.
PIR: A39118; CSHUB.
PIR: A40515; A40515.
PDB: 1CYN: 29-JAN-96.
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22742 MW;
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Best Local Similarity
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SEQUENCE FROM N.A.
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CYPB_MOUSE

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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
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-i- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-i- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDE BONDS IN OLIGOPEPTIDES.
--- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.
---- SUBJECLIULAR LOCATION: CYTODENSMIC.
---- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 49; DB 1; Length 208; 100.0%; Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4BBDF5AE40BAD3A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-94304830; PubMed-8031755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:97750; Ppib.
InterPro; IPRO02130; CSA_PPIase.
InterPro; PFO0150; pro_isomerase; 1.
PRINTS; PRO0153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Rotamase; Multigene family. 183 AA: 20193 MW: 23549C922828C533 CRC64;

SEQUENCE

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RESULT
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96276416; PubMed-8694762;
Page A.P., Macniven K., Hengartner M.O.;
"Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans.";
Blochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
1-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 11 (EC 5.2.1.8) (PPIASE)
                                                                                                                                                                                                                            100.0%; Score 49; DB 1; Length 212; 100.0%; Pred. No. 0.015;
                                                                                                                                                                                                                                                           0: Indels
                                                                                                                                                                 Cyclosporin; Isomerase; Rotamase; Multigene family.
SEQUENCE 212 AA; 22763 MW; 6F3DB547A2AE581B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             183 AA
                                                                                                                                                                                                                                                           0; Mismatches
entities requires a license agreement (or send an email to license@isb-sib.ch)
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EMBL; 266499; CAA91297.1; -.
HSPP; P505092; 3C78.
HORMPEP; T0187.4; CE03588.
InterPro; IPR002130; CSA_PP1ase.
Pfam; PF00160; pro_1somerase; 1.
PRONSTE; PR00153; CSA_PPIASE.1; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
                                                                                  Interior IPR002130; CSA_PPIBASE.
Pfam: PF00160; pro_isomerase: 1.
PRNTS: PR00123; CSAPPIBARASE.
PROSITE: PS00170; CSA_PPIBASE_1:
PROSITE; PS00770; CSA_PPIBASE_1:
PROSITE; PS00772; CSA_PPIBASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ROTAMASE) (CYCLOPHILIN-11).
CYP-11 OR T01B7.4.
                                         EMBL; S71018; AAB31350.1; -. HSSP; P05092; ZRMC. MIM; 123842; -.
                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                       HILLIIIII
86 KFHRVIKDF 94
                                                                                                                                                                                                                                                                                       1 KFHRVIKDF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                             CYPB_CAEEL
P52018;
                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
CYPB_CAEEL
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-91347379; PubMed-1652374; MEDLINE-91347379; PubMed-1652374; Medline-91347379; PubMed-1652374; Medline-91347379; Medline 1.L.; "Two cytoplasmic candidates for immunophilin action are revealed by affinity for a new cytoplain; one in the presence and one in the
                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
 Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:97751; Ppic.

MGD; MGI:97751; Ppic.

InterPro: IPRO00130; CSA_PPIase.

Priam; PF00160; pro_isomerase; 1.

PRINTS; PR00153; CSA_PPISMRASE.

PROSITE; PS00170; CSA_PPIASE_1; 1.

PROSITE; PS50072; CSA_PPIASE_1; 1.

PROSITE; PS50072; CSA_PPIASE_2; 1.

SEQUENCE 212 As; 22794 MW; C99E7AA5D0FA0486 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.8%; Score 44; DB 1; 100.0%; Pred. No. 0.14;
89.8%; Score 44; DB 1; 100.0%; Pred. No. 0.12;
                                                                                                                                                                212 AA
                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                PRT;
                100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M74227; AAA37511.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100. Matches 8; Conservative
                                Conservative
                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : A40047.
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-10090;
                                                                                      71 FHRVIKDF 78
                                                                                                                                                                                                                                                        (CYCLOPHILIN C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
                                                           2 FHRVIKDF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 FHRVIKDF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIIIIIII
87 FHRVIKDF
                                                                                                                                                                                                                                                                     PPIC OR CYPC.
                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A40047
                                                                                                                                                              CYPC_MOUSE
P30412;
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                                                                                                                                                 CYPC_MOUSE
                                Matches
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PPIB\_TREPA

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                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

A Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
Johnston M., Fulton L., Gattung S., Greco T., Kirsten J.,

Rucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
A Gunston D., Langston Y., Latrellle P., Mardis E.,
A Johnston L., Langston Y., Latrellle P., Mardis E.,
A Miles L., Taich S., Trevaskis E., Vaudin M., Vignati D.,
Riles L., Wilson R., Wohldman P., Waterston R.;
Submitted (SEP-1994) to the EMBL/Genbank/DDBJ databases.

C -! FUNCTION: PPIASES ACEERATE THE FOLDING OF PROTEINS.

C -- CATALYTIC ACITVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC

PEPTIDE BONDS IN OLIGOPEPTIDES.

C -! SUBMITH INTERACTS WITH RPD3.

C -! SUBMITARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                MEDLINE-97027304; PubMed-8873448;
Duina A.A., Marsh J.A., Gaber R.F.;
"Identification of two CyP-40-like cyclophilins in Saccharomyces cerevistae, one of which is required for normal growth.";
Yeast 12:943-952(1996).
                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE CPR6 (EC 5.2.1.8) (PPIASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 1; Length 371; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 AA; 42072 MW; 188666D94866DDDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPIASE, CYCLOPHILIN-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. w...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00153; CSAPPISMRASE,
PROSITE; PS00170; CSA_PPIASE_1; FALSE_NEG.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00160; pro_isomerase; 1. Pfam; PF00515; TPR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U48867; AAC49414.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U14913; AAB67445.1; -. HSSP; P05092; 1AWV. SGD; S0004206; CPR6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.88;
                                                                                                                  CPR6 OR YLR216C OR L8167.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity الاست
احد 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYP-40 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          somerase; Rotamase.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 FHRVIKDF 69
                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FHRVIKDF 9
                                                                                                (ROTAMASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                      "Identification of homologs for thioredoxin, peptidyl prolyl cis-trans isomerase, and glycerophosphodiester phosphodiesterase in outer membrane fractions from Treponema pallidum, the syphilis spirochete."; Infect. Immun. 65:4179-4189(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser C.M., Norits S.J., Weinstock G.M., White O., Sutton G.G., Odoson R., Gitnn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artlach P., Bowman C., Cotton M.D., Fujii C., Garland S. Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-97461344; PubMed-9317025;
Shevchenko D.V., Akins D.R., Robinson E.J., Li M., Shevchenko O.V.,
                                                                                                                                         5.2.1.8) (PPIASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.8%; Score 44; DB 1; Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isomerase, Rotamase; Complete proteome.
SEOUENCE 215 AA; 23272 MW; CCA1589C1F5A6D0B CRC64;
                                                                                                                                                                                                            Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                20-AUG-2001 (Rel. 40, Last annotation update) PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                      215 AA
                                                                                         (Rel. 37, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98332770; PubMed-9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISHRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.0
100.08; Fi
                                                                    (Rel. 37, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spirochete.";
Science 281:375-388(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U97573; AAC08055.1;
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                      STANDARD;
                                                                                                                                                              (ROTAMASE).
PPIB OR PPI OR TP0947.
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-NICHOLS;
                                                                                                                                                                                                                                                            NCBI_TaxID-160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TP0947;
                                                                  15-DEC-1998
                    PPIB_TREPA
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CYP6_YEAST
ID CYP6_Y
AC P53691
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204 AA.

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STANDARD;

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371 AA

PRT;

STANDARD;

CYP6\_YEAST P53691;

ô g 01-OCT-1996 (Rel. 34, Created)

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cyclophilin from Arabidopsis thaliana.";
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01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 5 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 26, Last sequence update)
01-FEB-1994 (Rel. 26, Last sequence update)
02-MG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROINL CIS-PRANS ISOMERASE, CHOROPLAST PRECURSOR
(EC. 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING
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MEDLINE-94179146; PubMed-8112503;
Lippuner V., Chou I.T., Scott S.V., Ettinger W.F., Theg S.M.,
Gasser C.S.;
"Cloning and characterization of chloroplast and cytosolic forms of
                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;

MEDILINE-96276416; Pubmed-8694762;

Page A.P., Macniven K., Hengattner M.O.;

"Cloning and blochemical characterization of the cyclophilin

homologues from the free-living nematode Caenorhabditis elegans.";

Blochem. J. 317:179-185 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-i- CATALVIIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPRIDE BONDS IN OLIGOPETIDES.
-i- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE PAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isomerase, Rotamase, Multigeme family,
SEQUENCE 204 AA; 22366 MW; 22ABB39AD1127BAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.8%; Score 43; DB 1;
88.9%; Pred. No. 0.21;
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                                                                                                                                                                      Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U31948; AAC47126.1; -. HSSP; P23284; 1CYN.
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                                                                                                                        Caenorhabditis elegans
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                                                                          (CYCLOPHILIN-5)
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-WAR-1992 (Rel. 21, Last sequence update)
01-WOV-1995 (Rel. 32, Last annotation update)
PEPPIDYL-PROINL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-51).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                         "Characterization of the cyclophilin gene family of Arabidopsis thaliana and phylogenetic analysis of known cyclophilin proteins."; Plant Mol. Biol. 35:873-892(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
D412AECBB8A5A3B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclosporin; Isomerase; Rotamase; Chloroplast; Transit peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 260;
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87.5%; Pred. No. 0.28;
tive 1; Mismatches
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Biol. Chem. 269:7863-7868(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam: PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE: PS00170; CSA_PPIASE_1; 1.
PROSITE: PS50072; CSA_PPIASE_2; 1.
                                                                              STRAIN=CV. COLUMBIA;
MEDLINE=98088013; PubMed=9426607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL138642; CAB71910.1; -. HSSP; P22384; ICYN. SWISS-2DPAGE; P34791; ARATH. InterPro; IPR002130; CSA_PPIASE.
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Matches 7; Conservative
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                                                                                                                                     ., Gasser C.S.;
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                                                 SEQUENCE FROM N.A
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TRANSIT
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1-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 6 PRECURSOR (EC 5.2.1.8) (PPIASE)
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-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                     Swinburne J., Palmer S.;
Swinburne J., Palmer S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PPTASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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PROSITE; PS0072; CSA_PPIASE_2; 1.
Isomerase: Rotamase: Multigene family.
SEQUENCE 523 AA; 58533 MW; 399967A6303989DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.7%; Score 41; DB 1;
77.8%; Pred. No. 1.4;
ive 2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 AA.
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NCBI_TaxID=6239;
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MEDLINE=96276416; PubMed=8694762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z46935; CAA85417.1; JOINED. EMBL; Z46935; CAA87053.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z36949; CAA87053.1; JOINED. HSSP; Q27450; 1A58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
SMART; SM00504; Ubox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002130; CSA_PPIase.
InterPro; IPR003613; Ubox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U36187; AAC06337.1; -. EMBL; Z36949; CAA85417.1; -.
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CYP-6 OR F42G9.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WormPep; F59E10.2; CE01596.
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Best Local Similarity 77.8
Matches 7; Conservative
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                                              STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KFHRVIKDF 9
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ID CYP6_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                              sequence and colocalizes with the calcium storage protein
calrediculin...
1 Cell Hiol. 116:113-125(1992).
-! FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-! CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGORPETIDES.
-! SUBCELLUAR LOCATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
-! SUBCELLUAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
HSSP: P23284: ICYN.
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P52012; 009548;
01-0CT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PEPTINIL-PROLYL CIS-TRANS ISOMERASE 4 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                                                                                                                                                                                                                       [2]
REVISIONS TO C-TERMINUS.
MEDLINE-92112948; PubMed-1530944;
Arber S., Krause K.-H., Caroni P.;
"S-cyclophilin is retained intracellularly via a unique COOH-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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MEDLINE-96276416; PubMed-8694762;
Page A.P., Macniven K., Hengartner M.O.;
"Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans.";
Biochem. J. 317:179-185(1996).
[1]
SEQUENCE FROM N.A.
MEDILNE-90300692; PubMed-2194066;
Iwai N., Inagami T.;
"Molecular cloning of a complementary DNA to rat cyclophilin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
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Live 1; Mismatches 1; Indels
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76D12AC3427FEF32 CRC64;
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PRNTX; PR00153; CSAPLISHRASE.
PROSITE; PS00170; CSA_PPIASE_1: 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                    Kidney Int. 37:1460-1465(1990).
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208
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CVP4_CABEL
COYP4_CABEL
COYP4_CABEL
DT 01-0CT
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                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
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15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYLERGLYL ISOMERASE (2P-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Onchocercidae; Brugia.
NCBI_TaxID-6279;
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MEDLINE-98218582; PubMed-9559680;
Taylor P., Page A.P., Kontopidis G., Husi H., Walkinshaw M.D.;
"The X-ray structure of a divergent cyclophilin from the nematode parasite Brugia malayi.";
FEBS Lett. 425:361-366(1998).
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084C5762917F958B CRC64;
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PEPTIDE BONDS IN OLIGOPEPTIDES.
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MEDLINE-96009642; PubMed-7547885;
Page A.P., Landry D., Wilson G.O., Carlow C.K.S.;
"Molecular characterization of a cyclosporin A-insensitive cyclophilin from the parasitic nematode Brugia malayi.";
Biochemistry 34:11545-11550(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.6%; Score 40; DB 1; Length 201; 77.8%; Pred. No. 0.8;
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                                                                                                                                                                                                                                                                                                           843 AA.
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MEDLINE-98318040; PubMed-9655334;
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Protein Sci. 7:1310-1316(1998).
[4]
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Matches 7; Conservative
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Q27450;
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SEQUENCE
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                                                                                                                          Biochemistry 39:592-598(2000).
--- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
--- ENZYME REGULATION: RELATIVELY INSENSITIVE TO INHIBITION BY CSA.
--- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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                       MEDLINE-20108543; PubMed-10642184;
Ellis P.J., Carlow C.K.S., Ma D., Kuhn P.;
"Crystal structure of the complex of brugia malayi cyclophilin and
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X-RAY CRYSTALLOGRAPHY (2.47 ANGSTROMS) OF 1-177.
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Job time: 654 sec
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Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSA_PPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1: 1.
PROSITE; PS00072; CSA_PPIASE_2; 1.
Isomerase; Rotamase; 3D-structure.
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Best Local Similarity
7; Conserve
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                                                                                                           cyclosporin A.";
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Pfam: PF00160; pro__somerase; 1.
PRIMTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
ISOMERASE; ROtamase; Signal; Cyclosporin; Endoplasmic reticulum.
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09d0w5 mus musculu
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027716 plasmodium
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                             473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                       January 15, 2002, 13:05:29
                                                                                                                                                                                                                                                  Listing first 45 summaries
                                      OM protein - protein search, using sw model
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098UE5
                                                                                                                                           Gapop 10.0 , Gapext 0.5
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O88541
Q9BVK5
Q9DCY1
Q9Y3C6
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                                                                                                                                                                                                                                                                                                                   sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                             sp_vertebrate:*
                                                                                                                                                                                                                              Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                           sp_archea:*
sp_bacteria:*
sp_fungi:*
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                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                sp_plant:*
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                                                                                                               KFHRVIKDF
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208
216
216
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166
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09fy98 arabidopsis
Q9ass6 arabidopsis
Q11004 schizosacch
076826 caenorhabdi
076824 brugia mala
09w0ç2 drosophila
079964 onchocerca
061300 dirofilaria
09u41 dictyosteli
09944 staphylococ
Q96847 onchocerca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen H., Li X.-L., Ljungdah L.G.;

A chen H., Li X.-L., Ljungdah L.G.;

A cyclophilin from the polycentric anaerobic rumen fungus Orpinomyces

T. A cyclophilin from the polycentric anaerobic rumen fungus Orpinomyces

T. Strain PC-2 is highly homologous to vertebrate cyclophilin B.";

Proc. Natl. Acad. Sci. U.S. A. 92.2587-2591(1995).

C. -! FUNCTION: PPLASES ACCELERATE THE FOLDING OF PROTEINS.

C. -! FUNCTION: PPLASES ACCELERATE THE FOLDING OF PROTEINS.

C. -! ENZYER ERCULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.

C. -! SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).

C. -! SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPLASE FAMILY.

REMBI: U17900; AAD04195.1;

REMBI: U17900; AAD04195.1;

Reddel: 20786: Unkp.1040; 20786.

R. Hichfplo: DENOV2130; CSA_PPIase.
                                                                                   09aqu0 oryza sativ
09fph5 arabidopsis
055035 rattus norv
                                                                                                                                               O9sihl arabidopsis
O9ni62 dictyosteli
                         070134 mus musculu
                                                 09gp41 echinococcu
09ch46 lactococcus
062190 caenorhabdi
                                                                                                                       013427 homo sapien
               trichophyto
 094190 emericella
093826 trichophyte
                                     O9vaw2 drosophila
                                                                                                                                   O9vawl drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEWBLrel. 06, Last sequence update)
01-JUN-2001 (TrEWBLrel. 17, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota: Fungi; Chytridiomycota; Neocallimasticales;
Neocallimasticaceae; Orpinomyces.
NCBL_TaxID-50059;
                                                                                                                                                                                                                                                                                                                                                                                                          203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.
MEDLINE-95223986; PubMed-7708690;
                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
                                                                                                                                                                             Q9ASS6
Q11004
O76826
O76824
Q9W0Q2
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Q9FPH5
Q55035
Q13427
                                                                                                                                                         09N162
09FY98
           093826
                                               Q9GP41
Q9CH46
O62190
                                                                                                                                               09SIH1
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061300
                                   29VAW2
                                                                                                                                   Q9VAW1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CYCLOPHILIN B) (ROTAMASE).
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PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.

CSA (POTENTIAL).
PREVENT SECRETION FROM ER

SIMILARITY). A5748C94305B8BE0 CRC64;

Length 216;

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23742 MW; 2D0410A07AA9E420 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9Y3C6;
01-NOV-1999 (TrEMBLrel. 12, Created)
                                                                                                                                                                                                                                                                Mus musculus (Mouse)
          216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 KFHRVIKDF 100
                                            Query Match
Best Local Similarity
                                                                                                                 92 KFHRVIKDF 100
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                                                                                          1 KFHRVIKDF 9
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          SEQUENCE
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Q9Y3C6
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AC Q9'
DT 01
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN B (EC 5.2.1.8).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mummalla; Eutherla; Rodentia; Solurognathl; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                          Rainer D. B., Doris P. A.;
"Cyclophilin B.";
"Cyclophilin B.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMDIC
--- PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
TRANS ISOMERASE FAMILY.
--- EMBL; AF071225; AAC25590.1; ---
HSSP; P23284; ICYN.
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B).
Homo saptens (Human).
Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 49; DB 11; Length 208; 100.0%; Pred. No. 0.068;
                    100.0%; Score 49; DB 3; Length 203; 100.0%; Pred. No. 0.066;
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                                             Indels
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TISSUE-SKIN, AND MELANOMA;
Strausberg R.,
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMpL; BC001125; AAH01125.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 AA; 22802 MW; 02408DFA7157218C CRC64;
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                                            0; Mismatches
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STRAIN-WISTAR-KYOTO; TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00160, pro_isomerase; 1.
PROUISS; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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Best Local Similarity 100.
Matches 9; Conservative
                                Best Local Similarity 100.
Matches 9; Conservative
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84 KFHRVIKDF 92
                                                                                   18 KFHRVIKDF 86
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                                                                    1 KFHRVIKDF 9
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                        Query Match
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STRAIN-C57BL/6J; TISSUE-KIDNEY;

STRAIN-C57BL/6J; TISSUE-KIDNEY;

STRAIN-C57BL/6J; TISSUE-KIDNEY;

KAWAI JJ., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishil Y.,

RAMAI JJ., Shinagawa T., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Salto R.,

RA Alzawa T., Marawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsud H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Rochim L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

Radi K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carrinoi P., de Bonaldo M.F.,

RIOSE P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,

Rochome P., Ring B., Ringwald M., Rodriguez I., Sakameto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K. H., Weltz C., Whittaker C., Whiming L.,

Nordone P., Robishida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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100.0%; Score 49; DB 4; L
100.0%; Pred. No. 0.071;
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Best Local Similarity 100...
9, Conservative
                                                                          Conservative
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205 AA.
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                        EMBL, AK004331, BAB23265.1; --
MGD, MGI:1916066; 1110060010Rik.
Interpro: IPR002139; CSA_PPPase.
Pfam; PF00166; Pro_isomerase; 1
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isomerase; Rotamase.
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52 KFHRIIKDF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                       Lin W.-C.; "Comparative gene cloning: Identification of novel human genes with Caenorhabditis elegans proteome as template."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRAIS ISOMERASE FAMILY.
EMBL: AFL51882; AAD3419-1; --
EMBL; BC003048; AAH03048.1; --
                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.0%; Score 48; DB 4; Length 166; 88.9%; Pred. No. 0.084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 AA; 18237 MW; 2872DC3336CD05E4 CRC64;
01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CGI-124 PROTEIN (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (reated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, P05092; ZRMC.
InterPro: IPR002130; CSA_PPIase.
Pfam: PF000160; pro_isomerase: 1.
PRIMTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1: 1.
PROSITE; PS50072; CSA_PPIASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/6J, TISSHE-EMBRYO;
MEDLINE-21085660; PathMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 1110060010RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 88.9%,
Best Local Similarity 88.9%,
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                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isomerase, Rotamase.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                     SEQUENCE FROM N.A.
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52 KFHRIIKDF 60
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                                                                                                                                                                                                                                                                                                                      TISSUE-LYMPHOMA;
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                                                                                                                              NCBI_TaxID=9606;
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Response From M. Carlot State 
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
Sasaki H., Sato K., Schombach C., Seya T., Sibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Mynshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001).
-!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 AA; 18237 MW; ASC5B04FE29C52C9 CRC64;
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Last annotation update)
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199 AA.

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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantea: Streptophyta: Embryophyta; Tracheophyta:
Spermatophyta; Magnoliophyta: eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicates; Brassicacees; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. COLUMBIA;

Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,

Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;

"Arabidopsis thallana chromosome II BAC T6A23 genomic sequence.";

Submitted (ccr.1998) to the EMBL/GenBank/DDBJ databases.

EMBL; ACO05499; AAC67345.1;

HSSP: P05092; ZCPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 AA; 21492 MW; FCC6DAB546C68C8C CRC64;
                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                         PUTATIVE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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01-MAY-1999 (TrEMBLrel. 10, Last seq
                                                                                                                                                            PRT;
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InterPro; IPRO02130; CSA_PPIsse.
Pfam: PF00160; pro_isomerase; 1-
PRINTS; PR00153; CSAPPISMRASE.
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                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                         1 KFHRVIKDF
                                                             84 KFHRVIKEF
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SEQUENCE
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                                                                                                                                                                                   Q92VJ4;
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                                                                                                                                                              Q92VJ4
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Kimmel B.E., Kodira C.D., Kraft C., Kravitž S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mateal B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., McDarry C., Morris J., Moshrefi A.,
Merkulov G., Milshina N.V., McDarry C., Morris J., Moshrefi A.,
Melson D.R., Nelson K. A., Nixon K., Nasskern D.R., Pacieb J.M.,
Nelson D.R., Nelson K. Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden Kinnos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Stropski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Stropski M.P., Smith T.,
K. Williams S.M., Woodage T., Worley K.C., Wu D., Yang A.H., Wang X.,
Williams S.M., Wassarman D.A., Weinstock G.M., Weissenbach J.,
K. The genome sequence of Drosophila melanogaster.";
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
C. -- CETALYTIC OF PROTEINS (BY STMLARTY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Amano T., Yoshizato K.;
"Isolation of genes involved in intestinal remodeling during anuran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus Laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibla; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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Best Local Similarity 88.9%; Pred. No. 0.2;
Matches 8; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.0%; Score 48; DB 5; Length 205; 88.9%; Pred. No. 0.11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF170328; AAK11503.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF6AD1CD1C2FB3E2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (FrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
peprIDYL-PROLYL CIS-TRANS ISOMERASE B (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flybase; FBgn0034753; CG2852.
InterPro; IPR002130; CSA_PPIase.
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11350 MW;
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Best Local Similarity 88.9°
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isomerase; Rotamase.
SEQUENCE 205 AA; 3
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104 AA;
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SEQUENCE
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                                                 Gaps
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  Length 199
                                                 Indels
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Last annotation update)
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Pred. No. 0.44;
91.8%; Score 45; DB 10; 88.9%; Pred. No. 0.39;
                                                                                                                                                                                                                                                        PRT; 145 AA.
                                              1; Mismatches
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Best Local Similarity
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Gaps

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Isomerase; Rotamase
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                                                                                                                                                                                    NCBI_TaxID-9606;
                                                                                                                                                                          2 FHRVIKDF 9
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                                                                                                                                                                                                                                                                                                                                                                              TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins
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  Gaps
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-!- FUNCTION: PEPTIDYL-PROINT CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGORPPTIDES.

-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.

FRANS ISOMERASE FAMILY.

EMBL; AF017999; AAB86601.1; -.

HSSP; P05092; ZCPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO ARABIDOPSIS THALIANA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                            STRAIN-HMI:IMSS:
Carrero J.C., Petrossian P., Acosta-Camarena E., Ostoa-Saloma P.,
Ortiz-Ortiz L., Laclette J.P.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
  ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.8%; Score 44; DB 5; Length 167; 100.0%; Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        18139 MW; DBA23FE5BB3290B2 CRC64;
                                                                                                                      Last sequence update)
Last annotation update)
  ;
                                                                                        167 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08; Pred. w.
  Mismatches
                                                                                                            Created)
                                                                                                                                                           Entamoeba histolytica.
Eukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF00160; pro_isomerase: 1.
PRNTMS; PR00153; CSAPLEMRASE.
PROSITE: PS00170; CSA_PPIASE_1: 1.
PROSITE; PS50072; CSA_PPIASE_2: 1.
ö
                                                                                                          01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2001 (TrEMBLrel. 17, CYCLOPHILIN (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 8; Conservative
8; Conservative
                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (P34791) (FRAGMENT)
Oryza sativa (Rice)
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                            33 FHRVIKDF 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||||
55 FHRVIKDF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4530;
                  2 FHRVIKDF 9
                                                                                                                                                                                                                                                                          STRAIN-HM1: IMSS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 FHRVIKDF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                      015729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09FW22
                                                                    RESULT 11
015729
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Matches
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MEDLINE-98230239; PubMed-9570313;
Teigelkamp S., Achsel T., Mundt C., Gothel S.F., Cronshagen U.,
Lane W.S., Marahiel M., Luhrmann R.;
"The 20kD protein of human [47,46.15] tri-snRNPs is a novel
cyclophilin that forms a complex with the U4/U6-specific 60kD and 90kD
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hsing Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M.,
Chen C.-S., Shaw J.-F.;
"Oryza sativa PAC P0036D10 genomics sequence, complete sequence.";
Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC073405; AAG03106.1;
InterPro: IPR002130; CSA_PPIase.
Pfam: PF00160; pro_isomerase; 1.
PRIMTS; PR00153; CSA_PPISMEASE.
PROSITE; PS50072; CSA_PPISMEZ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Horowitz D.S., Kobayashi R., Krainer A.R.; A new cyclophilin and the human homologues of yeast Prp3 and Prp4 form a complex associated with U4/U6 snRNPs."; RNA 3:1374-1387(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                           Length 173;
                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
U-SNRNP-ASSOCIATED CYCLOPHILIN (EC 5.2.1.8).
USA-CYP OR CYP-20.
                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                           89.8%; Score 44; DB 10;
                                                                                                                                                                                                                                                                                                                                                   0.53;
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                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF00160; pro_isome_ase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98067393; PubMed-9404889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002130; CSA_PPIase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF016371; AAC51927.1; -.
EMBL, AF036331; AAC60793.1; -.
EMBL, BC003412; AAH03412.1; -.
                                                                                                                                                                                                                                                                                                                         Ouery Match 89.89
Best Local Similarity 100.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-CHORIOCARCINOMA;
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65 FHRVIKDF 72
 2 FHRVIKDF 9
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                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishli Y.,
A Arakawa T., Hara A., Shibata K., Yoshino M., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arawa K., Izawa M., Nibila K., Kiyoswa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Rigis M., King B., Kochiwa H.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Sizuki R., Tomita M., Wagner L., Washio T.,
A Blake J., Bolfelli D., Bolunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wiltming L.,
A Wanshalland Y., Kawaji H., Kohtsuki S.,
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDE BONDS IN OLIGOPEPTIDES.
-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Purctional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutherla, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOLDING OF PROTEINS (BY SIMILARITY).
                                                                                      ;
0
                                                   Length 177;
                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 AA; 19208 MW; 566BCE6361E0F339 CRC64;
177 AA; 19208 MW; 566BCE6361E0F339 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-HEAD, EMBRYO, AND CEREBELLUM;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
483406FIRIK PROTEIN (1100001308RIK PROTEIN).
                                               Score 44; DB 4;
Pred. No. 0.54;
                                      89.8%; Scur.
100.0%; Pred. No. v...
0; Mismatches
                                                                                                                                                                                                                                                 177 AA
                                                                                                                                                                                                                                                   PRT;
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PR00153; CSAPPISMRASE.
PROSITE: PS00170; CSA_PPIASE_1: 1.
PROSITE: PS00072; CSA_PPIASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANS ISOMERASE FAMILY.

EMBL; AKO14665; BAE29493 1; -

EMBL; AKO03179; BAE22623.1; -

EMBL; AKO05202; BAE23880.1; -

EMBL; AKO05202; BAE3880.1; -

EMBL; MIST.9913150; 4833408F11R1k

InterPro; IPRO02130; CSA_PF1ase.
                                                                                                                                                                                                                                                                                                                                                          4833408F11RIK OR 1100001J08RIK.
                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                                               WCBI_TaxID=10090;
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65 FHRVIKDF 72
                                                                                                                          2 FHRVIKDF 9
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 SEQUENCE
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                                                                                                                                                                                                                                                                      090001;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Wioskins R.A., Galle K.F.,
Adams M.D., Celniker S.E., 11 P.W., Hoskins R.A., Galle K.F.,
Rananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle K.F.,
Rananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle K.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.
Bardon R.C., Rogers Y.H.C., Blazel R.G., Change M., Pielffer B.D.,
RA Man K.H., Doyle C., Barzer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Bardon R.C., Rogers Y.H.C., Blazel R.G., Chandre M. Pishankov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Butler H.J., Andrews-Fennkoh C., Baldwin D.,
RA Burtis K.C., Busam D.A., Butler H.J., Cadieu E., Center A., Chandre A.
Cherry J.M., Cavley S., Dablke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cavley S., Dablke C., Devenport L.B., Davies P.,
RA Cherry J.M., Cavley S., Dablke C., Ferraz C., Gens T., Dietz S.M.,
RA Cherry J.M., Cavley S., Davies M., Dugarn Rochs S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Barvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Marvey D., Helman T.C., Mel M.-H. Tbeyam C.,
RA Harris N.L., Marvey D., Helman T.C., Mel M.-H. Tbeyam C.,
RA Mount S.M., Woolpry C., McLeod M.P., McPherson D.L.,
RA Mount S.M., Woolpry C., McLeod M.P., McPherson D.L.,
RA Mount S.M., Woolbry C., McLeod M.P., McPherson D.L.,
RA Rimell B.R., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Richer E., Spradling A.C., Staplaton M., Skupski H.P., Smith T.,
Spier E., Spradling A.C., Staplaton M., Skupski H.P., Smith T.,
RA Richer E., Spradling A.C., Staplaton M., Skupski M.P., Sun B.,
Reiner E., Spradling A.C., Staplaton M., Skupski M., Welson D.Y.
RA Williams S.M., Woodege T., Worley K.C., Wu D., Yeng S., Zahon S., Zhen M., Wenges D.C.,
RA Penger E., Spradling A.C., Wu D., Welley D., Welley B.
                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Nooptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PROD153; CSAPPISHRASE.
PROSITE; PS50072; CSA_PPINSE_2; 1.
SEQUENCE 183 AA; 20182 MW; 1955CE187CB9E949 CRC64;
                                                                                      Last annotation update)
                                                              Last sequence update)
183 AA.
                                           Created)
PRT;
                                                                                                                                                                                                                                                                                                                                  MEDLINE-20196006; PubMcd-10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase: FBgn0033089; CG17266
                                    01-MAY-2000 (TrEMBLrel, 13, 01-MAY-2000 (TrEMBLrel, 13, 01-JUN-2001 (TrEMBLrel, 17, CG17266 PROTEIN.
PRELIMINARY;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  STRAIN-BERKELEY;
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Length 183;

DB 5; 0.56;

Score 44; Pred. No.

89.8%; 100.0%;

Query Match Best Local Similarity

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Gaps

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0; Indels

0; Mismatches

Conservative

Best Local Similarity Matches 8; Conserve

Query Match

89.8%; Score 44; DB 11; Length 177; 100.0%; Pred. No. 0.54;

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0; Gaps

0; Indels Matches 8; Conservative 0; Mismatches Search completed: January 15, 2002, 13:16:24 Job time: 655 sec 2 FHRVIKDF 9 ||||||||||| 71 FHRVIKDF 78 Oý Dp

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RESULT
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Human PRO4984 poly
Human colon cancer
Human cyclophilin
Human cyclophilin
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Human cyclophilin
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Human cancer assoc
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                                                                                                                                  January 15, 2002, 13:02:09; Search time 81.32 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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SIDSB/gcgdata/geneseqy/genescqp/AA1989_DAT:
SIDSB/gcgdata/geneseq/genescqp/AA1990_DAT:
SIDSB/gcgdata/geneseq/genescqp/AA1992_DAT:
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/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 522463
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                            522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
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AAB 7302
AAB 7302
AAB 7301
AAB 7301
AAB 7301
AAG 03983
AAG 03983
AAG 75471
AAY 69962
AAB 69962
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Maximum DB seq length: 2000000000
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49
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Match Length DB
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Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy. Human cyclophilin B peptide fragment #1. AAY69921 standard; peptide; 9 AA 11-APR-2000 (first entry) W09967288-A1 Homo sapiens 29-DEC-1999. AAY69921; AAY69921 

(SUMU ) SUMITOMO PHARM CO LTD. (ITOH/) ITOH K. 98JP-0178449. 25-JUN-1998;

99WO-JP03360.

24-JUN-1999;

WPI; 2000-116932/10. Itoh K, Gomi S;

Tumour antigen peptides derived from cyclophilin B for treatment and diagnosis of tumours  $\,$ 

Claim 4; Page 49; 64pp; Japanese

Gaps

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Length 9; Indels

Score 49; DB 22; Pred. No. 4.3e+05;

100.0%;

0; Mismatches

×85888×8

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9; Conservative
Query Match
Best Local Similarity
Matches 9; Conserv
                                                   1 KFHRVIKDF 9
                                                                 RESULT
AAB73302
                                                                                                                                AAG00090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes the novel use of interferons (IFNs) or DNAs capable of expressing the interferons and/or antiquency proteins (AP), antiquency peptides derived from the proteins or DNAs capable of expressing the antiquency or peptides, in the manufacture of an agent for induction of antiquen-specific T cells. The products of the invention have virucide and cytostatic activity and can be used for gene therapy or as inducers of antiquen-specific T cells. The action of interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic T cell (CTL) by administering an antiqueinc peptide in an incomplete Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or DNA encoding IFNs) are useful in the manufacture of a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inducing antigen-specific T cells in an individual who has been administered with {\sf AP} (or DNA encoding AP) or vice versa. The medicament is useful for the treatment or prophylaxis of a tumor or a viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of antigenic proteins, peptides, interferon or their encoding DNA, in the manufacture of an agent for the induction of antigen-specific {\tt T} cells -
           This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                     Tumor antigenic peptide; interferon; IFN; antigen-specific T cell; virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell; viral infectious disease; cyclophilin B; human.
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                                                                                                                                                                                                                                                                                                                                            Human cyclophilin B derived tumor antigenic peptide SEQ ID 16.
                                                                                                                   Length 9;
                                                                                                                                              Indels
                                                                                                                     100.0%; Score 49; DB 21; 100.0%; Pred. No. 4.3e+05;
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                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                 AAB46930 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamaoka T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUMU ) SUMITOMO PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUL-2000; 2000EP-0306263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-0207687.
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                     Query Match
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-193144/20.
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                                                                                                                                                                        1 KFHRVIKDF 9
                                                                               9 AA;
                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                         AAB46930;
                                                                                 Sequence
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                                                                                                                                                                                                                                                            Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; SEQ ID 4171; 71pp + CD-ROM; English.
                                                                                                                                                                                                       Human secreted protein, SEQ ID NO: 4171.
AAG00090 standard; Protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2000; 2000EP-0200610.
                                                                                                                                       (first entry)
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1033401-A2.
                                                                                                                                   06-0CT-2000
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                                                                   AAG00090;
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AAB73301 standard; protein; 216 AA.

AAB73301;

Human cyclophilin B (CypB). 22-MAY-2001 (first entry)

somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; gigantism; acromegaly; hyperprolactinaemia. Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding;

40200113113-A1.

22-FEB-2001

Homo sapiens.

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Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone
                                                                          Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; gigantism; acromegaly; hyperprolactinaemia; C-terminal deletion mutant; mutein.
                                                        Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.
AAB73302 standard; protein; 211 AA.
                                                                                                                                                                                                                                                                                                                                 Disclosure; Page -; 21pp; English.
                                                                                                                                                                                              10-AUG-2000; 2000WO-US21789.
                                                                                                                                                                                                                  99US-0149752
                                       (first entry)
                                                                                                                                                                                                                                    (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                       Clevenger CV, Rycyzyn MA;
                                                                                                                                                                                                                                                                         WPI; 2001-211249/21.
                                                                                                                                                        WO200113113-A1.
                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                  19-AUG-1999;
                                      22-MAY-2001
                                                                                                                                                                           22-FEB-2001
                    AAB73302
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The invention relates to a composition for modulating somatolactogenic function. Comprising cyclophilin B (CypB), a mutant of cyclophilin B (particularly a CypB mutant in which residues 2-12 of the mature protein are absent) or an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone (e.g., prolactin, growth hormone). The invention also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB levels in a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic function in the animal, and cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, is useful for inhibiting somatolactogenic function in the animal. A composition comprising cyclophilin B is useful in the treatment of immunosuppression, in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic composition comprising HVV infection, breast and prostate and prosecute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer, gigantism/acromegaly, and hyperprolactinaemia. The present sequence represents a human cyclophilin B C-terminal muttant, CypB-AIAKE. Note: The present sequence is not shown in the specification, but is derived from the wild-type CypB sequence shown on pages 17-18.
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/ Match 100.0%; Score 49; DB 22; Length 211; Local Similarity 100.0%; Pred. No. 0.039; hes 9; Conservative 0; Mismatches 0; Indels (
                                                                          1 KFHRVIKDF 9
    Query Match
                                  Matches
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RESULT AAB73301

AAB43878 standard; Protein; 291 AA. AAB43878; 9 AAB43878 ID AAB4 XX AC AAB4 RESULT

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The invention relates to a composition for modulating somatolactogenic function, comprising cyclophilin B (CypB), a mutant of cyclophilin B (particularly a CypB mutant in which residues 2-12 of the mature protein are absent) or an inhibitor of the interaction of cyclophilin B with a somatolactogenic relates to a method of identifying inhibitors of somatolactogenic also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for diagnosing diseases associated with abnormal somatolactogenic functions using CypB levels in a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic hormone, is useful for augmenting somatolactogenic function in the animal, and sucception of cyclophilin B with a somatolactogenic function in the animal. A composition comprising cyclophilin B with a somatolactogenic function in the animal. A composition comprising cyclophilin B with a somatolactogenic function in the treatment of immunosuppression, in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprising cyclophilin B mutant or a composition comprising cyclophilin B with a somatolactogenic function, breast and prostate cancer, glgantism/acromegaly, and hyperprolactinaemia. The present cancer, glgantism/acromegaly, and hyperprolactinaemia. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 17-18; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                              10-AUG-2000; 2000WO-US21789
                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYPE-) UNIV PENNSYLVANIA.
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Best Local Similarity 100.
Matches 9; Conservative
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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
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                                                                                                                                                                                            Human secreted protein, SEQ ID NO: 8064.
                        AAG03983 standard; Protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2000; 2000EP-0200610.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                               EP1033401-A2
                                                                                                                                       06-OCT-2000
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                                                                                   AAG03983;
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AAG03983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB4239. The proteins can have activities based on the tissues and cells the genes are expressed in Example of activities cinclude: cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antisthematic; antibaterial; antitificamatory; antithyrian antitificamatory; antithyrian antitificamatory; antithyrian; antitificamatory; antithyrian; cardiant; thrombolytic; coaquiant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides cand antiangiogenic. The polynucleotides and polypeptides and diagnosing pathological conditions. Polynucleotides and polypeptides and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agenthological conditions in the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, and disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and AAB44240 represent sequences used in the exemplification of
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                                                                                                                                                       diagnosis: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antidiabetic; antiasthmatic; antirheumatic; antibaterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipactive; thrombolytic; coagulant; nootropic; immune disorder; heematopoietic cell disorder; antidiamation; immune disorder; heematopoietic cell disorder; autoimmune disorder; haematopoietic cell disorder; autoimmune disorder; neaction; saft versus host disease; organ rejection; neurological disease; drug screening.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer
                                                                                                                                              Human; cancer associated gene; cancer antigen; detection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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                                                                                   Human cancer associated protein sequence SEQ ID NO:1323.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-2000; 2000WO-US05882.
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                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Ruben SM;
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N-PSDB; AAC78087.
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                              08-FEB-2001
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                             Gaps
                                                                                                                                                                                                                                                                                       Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
                             ;
DB 21; Length 113;
                             Indels
                             ;
98.0%; Score 48; DB 21; 88.9%; Pred. No. 0.032; Live 1; Mismatches
                                                                                                                                                                     AAU12175 standard; Protein; 166 AA.
                                                                                                                                                                                                                                                            Human PRO4984 polypeptide sequence.
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Sequence

Query Match Matches

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ANUIZI72-AAUIZ446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides. To link bloactive molecules to cells expressing PRO polypeptides, to anount because to cells expressing pro properties to modulate blological activities of cells expressing CRO polypeptides, and to detect the presence of mammalian lung, collon, cheast, prostate, rectal, cervical or liver tumours by comparing PRO, polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-labha (TNR-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation of human of any period of a cytokine from periopheral blood carillage, the proliferation of inner ear unitcular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide collecules involved in binding interactions. The polynucleotides encoding
cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deforge L, Desnoyers L, Filvaroff E, Ge
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig 8; 813pp; English.
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99WO-US30095.
99WO-US30911.
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2000WO-US13705
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Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tum
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                                                                           WO200140466-A2.
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16-DEC-1999;
16-DEC-1999;
20-DEC-1999;
30-DEC-1999;
06-JAN-2000;
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18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
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21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                           Gaps
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PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention.
N.B. Pages 66 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma,
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0
                                                                                                        Score 48; DB 22; Length 166; Pred. No. 0.048;
                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                Human colon cancer antigen protein SEQ ID NO:6235
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                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                           AAG75471 standard; Protein; 178 AA.
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                                                                                                    98.0%;
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                                                                                  Ouery Match
Best Local Similarity 88. ما المحالفة
المحالفة
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                                                    Sequence 166 AA;
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52 kfhriikdf 60
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178 AA;

Sequence

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Pakasu H, Gotoh M, Yamaoka T;
                                                                                                                                       (SUMU ) SUMITOMO PHARM CO LTD.
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88.9%;
                                                                                            24-JUL-2000; 2000EP-0306263.
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Best Local Similarity
The B; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA;
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                              Homo saplens
                                                   EP1074267-A1
                                                                                                                   22-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour antigen peptides derived from cyclophilin B for treatment and
                                Gaps
                                                                                                                                                                                                                   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
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        Length 178;
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Pred. No. 4.3e+05;
1; Mismatches 0; Indels
                              0; Indels
         Score 48; DB 22;
Pred. No. 0.052;
1; Mismatches 0;
                                                                                                                                                                                               Human cyclophilin B peptide fragment #42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 60; 64pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB46946 standard; peptide; 9 AA
                                                                                                                                AAY69962 standard; peptide; 9 AA.
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88.9%;
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  Query Match
Best Local Similarity 88.9°
Local Similarity 88.9°
Local Similarity 88.9°
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                      1 KFHRVIKDF 9
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1 kyhrvikdf
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                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                    AAY69962:
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This invention describes the novel use of interferons (IFNs) or DNAs capable of expressing the interferons and/or antigenic proteins (AP), antigenic opeptides derived from the proteins or DNAs capable of expressing the antigenic proteins or paptides, in the manufacture of an agent for induction of antigen-specific T cells. The products of the invention have virucide and cytostatic activity and can be used for gene therapy or as inducers of antigen-specific T cells. The action of interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic T cell (CTL) by administering an antigenic peptide in an incomplete Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or DNA encoding IFNs) are useful in the manufacture of a medicament for inducing antigen-specific T cells in an individual who has been administered with AP (or DNA encoding AP) or vice versa. The medicament is insertius disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of antigenic proteins, peptides, interferon or their encoding DNA, in the manufacture of an agent for the induction of antigen-specific {\bf T}
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virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell; viral infectious disease; cyclophilin B; human.
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Pred. No.4,3e+05;
L; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 19; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB56701 standard; Protein; 183
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A third mammalian cyclophilin, cyp C, was isolated from a CDNA library prepd. from the murine bone marrow derived stromal cell line AC 6. This cDNA was isolated from a substracted sub-library contg. Genes induced by treatment of the stromal cell line with interleukingers of (IL-1). The message levels for cyp C show a 2-3 fold induction by treatment with IL-1, and this cDNA exhibits a high level of homology with known cyclophilins. Cyp C is distinct from mammalian cyclophilins. Cyp C is distinct from mammalian cyclophilins A and B in both sequence and tissue distribution of expression. A fusion protein conque, e.g. amino acids i6-212 of cyp C possesses peptidyl-probyl isomerase (PPlase) activity which can be completely inhibited by addition of cyclosporin A (CsA). These cyp C fusion proteins can be used as ligands for the identification of intracellular proteins which together form high affinity associations. For example, the cyp C fusion protein binds to a protein of 77 kD in the absence of CsA, while in the presence fo CsA it no longer binds to this p77, but instead binds specifically to a protein of 55 kD, identified as calcineurin (U.S.S.N.07/740175).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyclophilin-like peptidyl prolyl cis-trans isomerase; CYPB; food processing; Endoplasmic retention signal; cis-trans isomerization; protein secretion; toxin; ADP-glucose pyrophosphorylase; glucanase; beta-1,4-endoglucanase.
                                                                                                                         Cyclophilin C polypeptide and nucleic acid encoding it - useful for screening a tissue-specific immunosuppressive agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.8%; Score 44; DB 14; Length 212;
100.0%; Pred. No. 0.38;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A. niger peptidyl-prolyl cis-trans isomerase (CYPB).
                                                                                                                                                                                      Claim 9; Page 46 + Fig 1; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= signal_peptide
24..212
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                    Weissman IL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
                                                             WPI; 1993-076431/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          niger.
                                                                                  N-PSDB; AAQ36841
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                    Friedman JS,
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAP16506 to AAP16514 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                        Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclophilin C; bone marrow; stromal cell line; AC 6; interleukin-1; IL-1; cyp A; cyp B; peptidyl-prolyl isomerase; PPIase; cyclosporin A; CsA; ligand; calcineurin.
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                                                                                                                                                                                                                                                                                                                                                  disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR32353 standard; Protein; 212 AA.
                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                    08-MAR-2000; 2000WO-US05988
                                                                                               99US-0124270
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Best Local Similarity 100...
8; Conservative
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                                                                                                                                                                                                                                        WPI; 2000-587513/55.
N-PSDB; AAF15904.
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                                                                                           12-MAR-1999;
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             21-SEP-2000
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AAR32353 ID AAR3 RESULT

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99US-0144814.
99US-0145086.
99US-0145088.
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
07-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
16-MAY-1999;
19-MAY-1999;
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21-MAY-1999;
22-MAY-1999;
22-MAY-1999;
23-MAY-1999;
01-JUN-1999;
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28-JUN-1999;
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  This sequence shows Aspergillus niger cyclophilin-like peptidyl prolyl cistrans isomerase (CYPB). CYPB is capable of catalyzing the cistrans isomerization of a peptide bond on the N-terminal side of proline residues in polypeptides. CYPB are useful in methods for increasing the yield of secreted polypeptides from cells. The secreted polypeptides may be enzymes (such as chymostin, thaumatin or alpha-squarcossidase) that can be used in food processing, a pest toxin, adenosine diphosphate (ADP)-glucose pyrophosphorylase, a glucanase or beta-1,4-endoglucanase.
                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                  0; Gaps
                                                  New peptidyl prolyl cis-trans isomerase, designated CYPB, from Aspergillus niger, useful in methods for increasing the yield of secreted polypeptides, such as enzymes used in food processing, from cells
                                                                                                                                                                                                                              89.8%; Score 44; DB 21; Length 212; 100.0%; Pred. No. 0.38; 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 17119.
                                                                                                    Claim 13; Page 47-48; 52pp; English,
                                                                                                                                                                                                                                                                                                                                 AAG16463 standard; Protein; 252 AA
                                                                                                                                                                                                                                         ilarity 100.0%; Pr
Conservative 0;
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990S-0126264
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           Derkx PMF, Madrid SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
                             WPI; 2000-293167/25.
                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
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05-MAR-1999,
23-MAR-1999,
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16-APR-1999,
116-APR-1999,
123-APR-1999,
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PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145087.
PR 23-JUL-1999; 99US-0145087.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145146.
PR 27-JUL-1999; 99US-0145146.
PR 27-JUL-1999; 99US-0145146.
PR 27-JUL-1999; 99US-014518.
PR 27-JUL-1999; 99US-014518.
PR 27-JUL-1999; 99US-014518.
PR 02-AUG-1999; 99US-0147303.
PR 02-AUG-1999; 99US-0147303.
PR 03-AUG-1999; 99US-0147303.
PR 03-AUG-1999; 99US-0147303.
PR 03-AUG-1999; 99US-0147303.
PR 03-AUG-1999; 99US-0147303.
PR 13-AUG-1999; 99US-0147303.
PR 27-AUG-1999; 99US-0149318.
PR 27-AUG-1999; 99US-0149318.
PR 27-AUG-1999; 99US-0149328.
PR 27-AUG-1999; 99US-0151308.
PR 27-AUG-1999; 99US-015308.
PR 27-AUG-1999; 99US-
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PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160814.
PR 22-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160816.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161405.
PR 26-OCT-1999; 99US-0161350.
PR 26-OCT-1999; 99US-0161350.
PR 28-OCT-1999; 99US-0161350.
PR 28-OCT-1999; 99US-0161351.
PR 28-OCT-1999; 99US-0161992.
PR 28-

Search completed: January 15, 2002, 13:05:26 Job time: 197 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O15729 antamodes h	Offw22 orwan satin	Od3447 homo sanien	Ogonia ana Discult	0.2694 toxon again	00v9h9 drosoph:19	Ogd868 mis misculu	001490 mus muscuiu	062190 Orpinomyces	OOKIDA CREMOLINADAL	O89541 retting north	Ognens rathers not v	027716 plaemodium		OGNAPS CHICATOR	Oddow1 mine misson 1:		0440/3 cacnypieus	O93826 trichophyto	O9aquo oryza sativ
SUMMARIES	αı	015729	) O9FW22	043447	090007	026994	696460	090868	001490	062190	09W227	088541	090605	027716	094190	O9BVK5	09DCY1	044073		093826	09AQU0
	Query Match Length DB	167 5	173 10	177 4	177 11	179 5	183 5	188 · 11	203 3	204 5	205 5	208 11	210 5	210 5	214 3	216 4	216 11	2000		770 3	231 10
ф	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	000	100.0	100.0
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09FY98	09ASS6	Q9FPH5	Q9GP41	055035	013427	093970	Q9HFU2	однепз	098UE5	046022	065191	O9ATCS	09N717	000845	P73789	002614	097766	0911983	096878	00000	201000	036877	094611	09U1B6	Q9N162	Q9D0W5
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100.0	100.0	100.0	0.86	0.86	98.0	96.0	96.0	96.0	92.0	92.0	90.0	90.0	0.06	0.06	0.06	90.0	0.06	90.0	0.06	0 06		0.0	90.0	90.0	0.88	88.0
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## ALIGNMENTS

RESULT

	015729 PRELIMINARY; PRT; 167 AA. 015729;	1998 (TrEMBLrel.	(TrEMBLrel. 05, Last	(TrEMBLrel. 17, Last	CYCLOPHILIN (EC 5.2.1.8).	CIPHI.		Eukaryota; Entamoebidae; Entamoeba.	NCBI_TaxID=5759;		SEQUENCE FROM N.A.	STRAIN=HM1;IMSS;	Carrero J.C., Petrossian P., Acosta-Camarena E., Ostoa-Saloma P.,		Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.		SEQUENCE FROM N.A.	STRAIN-HM1:IMSS;	Carrero J.C., Petrossian P., Acosta-Camarena E., Ostoa-Saloma P.,		Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.	- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE	FOLDING OF PROTEINS (BY SIMILARITY).	_	PEPTIDE BONDS IN OLIGOPEPTIDES.			EMBL; AF017993; AAB86601.1;	HSSP; P05092; 2CPL,	InterPro, IPR002130; CSA_PPIase,	Pfam; PF00160; pro_isomerase; 1.	PRINTS; PR00153; CSAPPISMRASE.	PS00170;	ທ		101 VOT
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Query Match

Length 167; DB 5; Score 50; 100.08;

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SEQUENCE
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
SIMILAR TO ARRIDOFSIS THALIANA PEPTIDYL-PROLYL CIS-TRANS ISOMBRASE
(P34791) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
HSING Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M.,
HSING Y.-S., Shaw J.-F.;
Chora sativa PAC P0036D10 genomics sequence, complete sequence.";
Submitted (SEP-2000) to the EMBL/Genbank/DDBJ databases.
EMBL: AC073405; AAG03106.1; -.
InterPro.; IPR00150; JOSA_PPIASE.
PRINTS; PR00160; pro_isomeraes.
PRINTS; PR00160; pro_isomeraes.
PROSTTE; PS50072; CSA_PPISMRASE.
PROSTTE; PS50072; CSA_PPISMRASE.
NOWN TER 173 173-1... NORNAGREGEB9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (Rice).
Eukaryoch: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnollophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.
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                                                         Indels
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
U-SRNP-ASSCCIATED CYCLOPHILIN (EC 5.2.1.8).
USA-CYP OR CYP-20.
Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                            173 AA.
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                                                             9; Conservative
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                              Best Local Similarity
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A STAIN—CSTBL/GG; TISUE-HEAD, EMBRYO, AND CEREBELLUM;

REDLINE—21085660; PubMed=11217851;

REDLINE—21085660; PubMed=11217851;

RA ARAWA T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishili Y.,

RA Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alzawa K., Izawa M., Nishi K., Kiyoswa H., Rondo S., Yamanaka I.,

RA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

RA Saito T., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Richi P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,

RA Richi P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,

RA Schriml L.M., Saubili F., Sucuki R., Tomita M., Wagner L., Hashlo T.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Cariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Grach R., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Buxuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Haynahaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Haynahaw-Boris A. Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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cyclophilin that forms a complex with the U4/U6-specific 60kD and 90kD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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01-JUN-2001 (TrENBLrel. 17, Last sequence update)
01-JUN-2001 (TrENBLrel. 17, Last annotation update)
4833408F11RIK PROTEIN (1100001J08RIK PROTEIN).
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InterPro; IPR002130; CSA_PPIASE.
Pfam; PF00160; pro_lsomerase; 1.
PRNUTS; PR00151; CSA_PPISMASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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Best Local Similarity 100.
Matches 9; Conservative
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                                                  proteins.";
RNA 4:127-141(1998).
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                                                                                                                                                           SECUENCE FROM N.A
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1 DFMIQGGDF 9
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High K.P., Joiner K.A., Handschumacher R.E.;
High K.P., Joiner K.A., Handschumacher R.E.;
Isolation, CDN sequences, and biochemical characterization of the major cyclosporin-binding proteins of Toxoplasma gondii.";
J. Blol. Chem. 269:9105-9112(1994).
II. FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
II. CATALVIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
II. ENZYME REGULATION: BINDS CCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
II. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                PEPTIDE BONNS IN OLIGOPBETIDES.
--- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last amnotation update)
01-VUN-2001 (TrEMBLrel. 17) Last amnotation update
01-TUN-2001 (TrEMBLRel. 17) Last amnotation update)
PEPTIDYL-PROLIC (IS-TRANS ISOMERASE PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
-!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDYL-PROLYL CIS-TRANS ISOMERASE. DB392502CC0DB6CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                       100.0%; Score 50; DB 11; Length 177; 100.0%; Pred. No. 0.037; Live 0: Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                              19208 MW; 566BCE6361E0F339 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 AA.
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                                                                                            PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
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RRNYS; PR00150; CSAPPISMRASE.
PROSITE: PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                              Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR002130; CSA_PPIase.
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                                                                                   TRANS ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                             71 DFMIQGGDF 79
                                                                                                                                                                                                                                                                                                                                                                                           1 DFMIQGGDF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toxoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toxoplasma |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-RH;
                                                                                                                                                                                                                                                                              SEQUENCE
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RX STRAIN-BERELELY;
RX Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Holt R.A., Eshancer M., Henderson S.N.,
RA George R.A., Lewis S.E., Holt R.A., Eshancer M., Henderson S.N.,
RA Brandon R.C., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Bazer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., Barendale J., Bayaktaroglu L., Beasley E.M.,
RA Ballew R.M., Basun A., Barendale J., Bayaktaroglu L., Beasley E.M.,
Rabril J.F., Agbayani A., Barendale J., Bayaktaroglu L., Beasley E.M.,
Rabril J.F., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchen M.R., Bouck J., Brokstein P., Bortter S. M.,
Borkova D., Botchen M.R., Bouck J., Brokstein P., Bortles P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavigelista C.C., Ferraz C., Perriera S., Pleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Perriera S., Pleischmann M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Perriera S., Pleischmann M.,
RA Hostin D., Houston K.A., Howlend T.J., Hernandez J.R., Houck J.,
Alali M., Kalush F., Katpen G. H., Ka Z., Kennison J.A., Kethum K.A.,
Alali M., Kalush F., Katpen G. H., Ka Z., Kennison J.A., Kethum K.A.,
Alali M., Kalush F., Katpen G. H., Kraft C., Sauders R., Pollar S., Spier E., Spradling A.C., Stapleton M., Strong R., Pollar S., Spier E., Spradling A.C., Stapleton M., Strong R., Shue B.C., Siden-K
                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophilia.

NCBL_TAXID-7227;
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                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                             183 AA.
                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50072; CSA_PPIASE_2; 1
SEQUENCE 183 AA; 20182 MW; 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00160; pro_isomerase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002130; CSA_PPIase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0033089; CG17266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS, PRO0153; CSAPPISMRASE
                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, CG17266 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE003789; AAF57375.1;
                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
73 DFMIOGGDF 81
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Length 183;

Score 50; DB 5; Pred. No. 0.039;

100.0%; 100.0%;

Best Local Similarity

Query Match

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Gaps

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0; Indels

Mismatches

0;

Conservative

Query Match Best Local Similarity Matches 9; Conserv

100.0%; Score 50; DB 5; Length 179; 100.0%; Pred. No. 0.038;

5.2.1.8) (PPIASE)

Matches

ò a RESULT 090868

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MEDLINE-94150718; PubMod-7906398; M. Habrison R., Baynes C., Berks M., Aliscough R., Adderson K., Borderson T., Connell M., Copsey T., Cooper J., Coulson A., Craxton M., Pear S., Du Z., Durbin R., Favello A., Fulton L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_FaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prant, PPOJIGO, pro_isomerase; 1.
Prants; PRODISO; CSAPPISMRASE.
PROSITE; PSO0170; CSA_PPIASE_1; 1.
PROSITE; PSS0072; CSA_PPIASE_2; 1.
Isomerase; Rotamase; Signal; Cyclosporin; Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 50; DB 3; Length 203; 100.0%; Pred. No. 0.044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSA (POTENTIAL).
PREVENT SECRETION FROM ER
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                                                                                                                                     Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
Neocallimasticaceae; Orpinomyces.
NCBI_TaxID=50059;
            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDNI-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.
MEDLINE-95223986; Pubmed-7708690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, U17900; AANO4195.1; -...
HSSP, P22384; ICYN,
Mendel; 20786; Unkp.1040,20786.
Interpro; IPR002136; CSA_PPIBSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21969 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-JUN-2001 (TrEMBLrel. 17, CYP-5 PROTEIN (EC 5.2.1.8)
                                                                                             (CYCLOPHILIN B) (ROTAMASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                   PC-2
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Best Local Similarity
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062190
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K AWAI J. S. Shingawa A. Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arawa T., Hara A., Fukunishi Y., Ronno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aitor K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuchi P., Lewis S., Matsud H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuchi P., Lewis S., Matsud H.F., Straubi F., Staubi B., Boffelli D., Bojuga N., Carninci P., de Bonaido M.F.,

Blake J., Boffelli D., Bojuga N., Carninci P., de Bonaido M.F.,

Rownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Rowdone P., Ring B., Rigwald M., Rodriguez I., Sakamoto N.,

Nordone P., Ring B., Rigwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Willing L.,

Nushaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.;
*Punctional annotation of a full-length mouse cDNA collection.*;
*Punctional annotation of a full-length mouse cDNA collection.*;
*Luce 409:665-690(2001).
*I- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOUNCTION: PEPTIDE (BY SIMILARITY).
*I- CALLING ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteléostoml;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID*10090;
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  Indels
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                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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  Mismatches
                                                                                                                                                                                                                 Created)
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PRIMYE: PR00123; CSAPPISMRASE.
PROSITE: PS00170; CSA_PPIASE_1: 1.
PROSITE: PS50072; CSA_PPIASE_2: 1.
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InterPro; IPR002130; CSA_PPIASE.
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Best Local Similarity 100.0%;
Matches 9; Conservative 0,
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                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 2010111B15RIK PROTEIN.
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  9; Conservative
                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
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71 DFMIQGGDF 79
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                                                               11111111
77 DFMIQGGDF 85
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                                        1 DFMIQGGDF 9
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SEQUENCE
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InterPro; IPR002130; CSA_PPlase.
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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RA Addams M.D., Celniker S.E., ILI P.W., Hoskins R.A., Galle R.F.,
RA Addams M.D., Celniker S.E., Richards S., Ashburner M., Hendelerson S.N.,
Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Batton R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baddwin D.,
RA Abril J.F., Benos P.V., Berman B.P., Brokstein P., Brottler P.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., bew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., bew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gales T., M.M., Glasser K.,
RA Harris N.L., Harvey D., Hennandez J.R., Houck J.,
RA Harris N.L., Harvey D., Hennand T.J., Wei M.-H., Ibegwam C.,
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Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mcmurlay A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaudinan R., Materston R., Watson A., Weinstock L., Wilkinson-Sprea J., Wohldman P., "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eurygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophilidae; Orosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                  -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.

EMBL: 292784; CAB07192.1; -.
                                                                                                                                            -:- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
-:- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 50; DB 5; Length 204; 100.0%; Pred. No. 0.044;
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                204 AA; 21927 MW; 6216192BFE1FB493 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEWBLrel. 13, Last Sequence update)
01-JUN-2001 (TrEWBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                       PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                           HSSP; P23284; ICYN.
InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; Pro_isomerase; 1.
PRINTS: PR00153; CSA_PPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100...
Per Py Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                 Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                    Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 DFMIQGGDF 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DFMIQGGDF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG2852 PROTEIN.
                                                                                                                   elegans."
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9W227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09W227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
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A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lansko P., Lei Y., Levitzky A.A., Liu Z., Linng Y., Lin X., Liu X., Martei B., McIntosh T.C., McLeod M.P., McPherson D., And McIntosh T.C., McLeod M.P., McPherson D., Anderkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Mursh D.R., Palson D.L., And Reloch E., Molson K.A., Nivon K., Niusskern D.R., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Rennert K., Remington K., Saunders R.D.C., Scheeler F., Shan H., Shue B.C., Slden-Klamos I., Simpson M., Strong R., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Smith T., Anger E., Worley K.C., Wu D., Yang S., Yao O.A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang G., Zhao G., Zhang G., Physics B.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.
EMBL; AEDOMSTAS9, AFR46873.1; -.
HSSP, P22384; ICYN.
FlyBase; FBgn0034753; CG2852.
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-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.

EMBL; AFO71225, AAC25590.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22199 MW; A9CEF88B1CC813F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NUV-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN B (EC 5.2.1.8).
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STRAIN=WISTAR-KYOTO; TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDE BONDS IN OLIGOPEPTIDES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISNIASE. PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002130; CSA_PPlase.
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01-MAY-1999 (
01-JUN-2001 (
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                                                                                                                                                                 Reddy G.R.;
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01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMBRASE PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
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                                                                                                                                             100.0%; Score 50; DB 11; Length 208; 100.0%; Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                     Indels
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                                                                       Isomerase; Rotamase. – – SEQUENCE 208 AA; 22802 MW; 02408DFA7157218C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN.
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                                                                                                                                                                                                                                                                                                                                                      210 AA.
                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR002130; CSA_PPIase.
Interpro; IPR002114; PTS_HPT_ser.
Pfam; PP00160; PTS_HPT_ser.
PRINTS; PR00153; CSAPPISMRASE.
PROSTIE: PS00170; CSA_PPIASE.
PROSTIE: PS00707; CSA_PPIASE.
PROSTIE: PS00589; PTS_HPR_SEZ; UNKNOWN_1.
Pfam; PF00160; pro_isomerase; 1.
PROUTS; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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SEQUENCE 210 AA;
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                                                                                                                                                                                                                                               91 DFMIQGGDF 99
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Q9U6U5
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PEPTIDE BONDS IN OLIGOPETIDES.

- PEPTIDE BONDS IN OLIGOPETIDES.

- DEVELOPMENTAL STAGE: EXPRESSED IN ALL ERYTHROCTTIC STAGES, BUT HIGHEST LEVEL OF EXPRESSED IN ALL ERYTHROCTTIC STAGE.

- SIMILARITY BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

R HSSP: POSO32: ACA6975.1.

R INTERPRO IPRO01310; CSA_PPIASC.

R INTERPO: IPRO01310; CSA_PPIASC.

R PROSITE; PSO0170; CSA_PPIASE.

T SIGNAL

T SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Gene sequence tags from Plasmodium falciparum genomic DNA fragments prepared by the 'genease' activity of mung bean nuclease."; Proc. Natl. Acad. Sci. U.S.A. 90:9867-9871(1993).

Proc. Natl. Acad. Sci. U.S.A. 90:9867-9871(1993).

-I. FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

-I. CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                         "Cloning and characterization of a Plasmodium falciparum cyclophilin
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-94022193; PubMed-8234327;
Reddy G.R., Chakrabarti D., Schuster S.M., Ferl R.J., Almira E.C.,
Dame J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOSEPH J.D., Means A.R.;
"Aspergillus nidulans cyclophilln B gene (CypB).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: PEPTIDYL-PROLYL. CIS-TRANS ISOMERASES ACCELERATE THE POLDING OF PROTEINS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella,
                                                                        Enkaryota: Alveolata; Alscomplexa: Haemosporida; Plasmodium.
NCBI_TaxID=36329, 57267, 137071;
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778A359F0FD47D26 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                         gene that is stage-specifically expressed."; Mol. Biochem. Parasitol. 73:111-122(1995).
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plasmodium falciparum (1solate 3D7),
Plasmodium falciparum (isolate Dd2), and
Plasmodium falciparum (1solate hb3).
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24049 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Tremberel. 10, C
(Tremberel. 10, I
(Tremberel. 17, I
A B (EC 5.2.1.8).
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210 AA;
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Best Local Similarity
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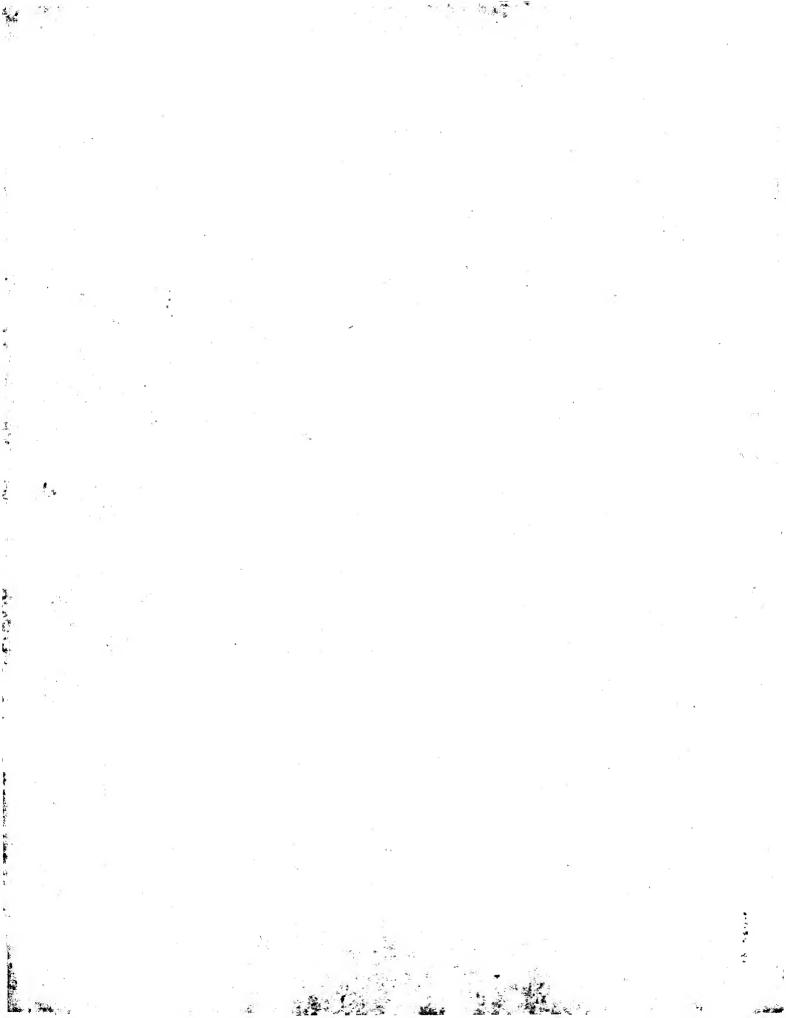
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           Gaps
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLRel. 17, Last annotation update)
01-JUN-2001 (FREMBLRERS B (CYCLOPHILIN B).
HOMO sapiens (Human)
EUKaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
MAMMMalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
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100.0%; Score 50; DB 3; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels
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Query Match

Best Local Similarity 100.0%; Pred. No. 0.047;

Matches 9; Conservative 0; Mismatches 0; Indels
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TISSUE-SKIN, AND MELANOMA;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; BC001125; AAH01125.1; -..
ISOMERASE.
SEQUENCE 216 AA; 23742 MW; 2D0410A07AA9E420 CRC64;
                                                                                                                                                        Isomerase; Rotamase. — SEQUENCE 214 AA; 23406 MW; 5A4DCFAEBE529DFA CRC64;
                                                                                                                                                                                                                                                                                                                                          PRT; 216 AA.
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99 DFMIQGGDF 107
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Q9BVK5
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Search completed: January 15, 2002, 13:16:25 Job time: 656 sec



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Ouery Match 100.0%; Score 50; DB 2; L
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0;
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MOLECULE TYPE: protein
US-08-482-728A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 126 amino TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-142-897-7

US-08-482-728A-16

US-08-482-728A-16

US-08-145-995A-14

US-08-145-995A-14

US-08-145-995A-14

US-08-145-995A-3

US-08-145-995A-3

US-08-145-995A-3

US-08-145-995A-3

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US-08-411-747-3

US-08-411-747-3

US-09-134-852-3

US-09-134-852-3

US-09-134-852-3

US-09-134-852-3

US-09-134-852-3

US-09-134-852-3

US-09-1445-956-6

US-08-451-747-21

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US-08-451-747-21

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US-08-482-728A-11
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-08-145-995A-6
-08-451-747-6
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US-08-451-747-5
US-09-134-852-5
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Maximum Match 100%
Listing first 45 summaries
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Perfect score:
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Maximum DB
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    Sequence 6, A Sequence 7, A Sequence 7, A Sequence 7, A Sequence 15, Sequence 15, Sequence 15, Sequence 11, Sequence 11, Sequence 7, A Sequence 11, Sequence 7, A Sequence 9, A Sequence 14, Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Fayan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
NUMBER OF SEQUENCES: 21
CORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fletch, Hobbach, Test, Albritton
ADDRESSEE: Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONTENT AFPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: 511va, Robin M.
REFERENCE/DOCKET NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 38,304
TELEPHONE: (415) 781-1989
TELEPAX: (415) 339-3249
TELEPAX: 910 277299
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 10, Application US/08482728A
; Patent No. 5968802
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884.0
884.0
884.0
880.0
880.0
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78.0
78.0
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Gaps .; 0

Length 126; Indels

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ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ...ms DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/142,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 212 amino acids
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEC ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 10v.v
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APPLICATION NUMBER: U
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STATE: California
                    STREET: ONe Market P
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
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                                                                                                        Sequence 7, Application US/08142897

Patent No. 5447852

GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Friedman, Jeffrey S.
PAPLICANT: Welsman, Irving L.
TITLE OF INVEWTION: No. 5447852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
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                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECHMONICATION INFORMATION:
TELECHMONE: 415-326-2400
TELECHMONE: 415-326-2402
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5447852
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
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Best Local Similarity 100.
Matches 9; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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      42 DFMIQGGDF 50
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                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                     94105
                                                                                                                                                                                                                                                                                                                             CITY: Sar
STATE: Ce
COUNTRY:
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US-08-142-897-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Fisher, Donald
APPLICANT: Payan, Donald
APPLICANT: Payan, Donald
APPLICANT: Payan, Donald
TITLE OF INVENTION: NO. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: 6 Herbert
ADDRESSEE: 6 Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: Dunn, Tracy D.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECHONE: 415-326-2400
TELEPHONE: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                               5490A-92-1
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Gaps
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0
                                                                                                                                                                                                                                                                  Sequence 14, Application US/08145995A
Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: OMBOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN
                                                                DB 1; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 162;
                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Floppy disk
COMPUTER: The PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
ATTORNEY APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                Score 48; DB 1;
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 1;
Pred. No. 0.13;
1; Mismatches
                                                                                                     1; Mismatches
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US-08-451-747-14
US-08-451-747-14
Sequence 14, Application US/08451747
Patent No. 5821107
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
                                                              96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 14
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88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 96.09
Best Local Similarity 88.99
Matches 8; Conservative
                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-145-995A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: un
                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                               111:1111
57 DFMLQGGDF 65
                                                                                                                                      1 DFMIOGGDF 9
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                                                                                                                                                                                                                                                    US-08-145-995A-14
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        US-08-142-897-9
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Patent No. 5447852
GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Friedman, Irving L.
TITLE OF INVENTION: And Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                               DB 2; Length 126;
                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: 0S/08/142,897
      ATTOWNER, NAME: SILVA MAME: SILVA MAME: SILVA MAME: SILVA MAME: ALEISTRATION NUMBER: 88,304
RECISTRATION NUMBER: A-61230/DJB/RMS TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 398-3249
TELER MAME: 910 27/299
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH: LES AMINO acids
                                                                                                                                                                                                                                                                                                                                             Score 48; DB 2
Pred. No. 0.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PROR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AGC-1991
ATORNEY/AGENT INFORMATION:
NAME: DUIN, TRACY D.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490-92-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                             96.0%;
ATTORNEY/AGENT INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-482-728A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: unkr
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                              42 DFMLQGGDF 50
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US-08-142-897-9
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Length 162;
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APPLICANT: Pisher, Joseph
APPLICANT: Payan, Donald
APPLICANT: Payan, Donald
APPLICANT: Payan, Donald
CORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: & Herbert
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: SILVA, RODII M,
REGISTRATION NUMBER: 38.304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFX: (415) 398-3249
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 3;
Pred. No. 0.13;
1; Mismatches
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                                                                                          FILING DATE: 29-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: DECENT.
                     APPLICATION NUMBER: US/09/134,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08482728A
Patent No. 5968802
                                                                                                                                                           NAME: RESNICK, DAVID S.
REGISTRATION UNDHER: 34235
REFRENCE/DOCKET NUMBER: 43401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELER: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                 162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.5.
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
: MOLECULE TYPE: protein
US-09-134-852-14
                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111:1111
57 DFMLQGGDF 65
                                                              CLASSIFICATION:
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                                           FILING DATE:
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STREET: 130 WATER STREET
CITY: BOSTOW
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
WEDDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTION:
COMPUTER: TEM PC COMPACTION:
COMPUTER: TEM PC COMPACTION:
SOFTWARE: PatentIn Release #1.0, Version #1.25
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC TITLE OF INVENTION: COMPOUNDS NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES GRECORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC STREET: 32 TOZER ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/09134852
Patent No. 6127148
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOFILLDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 162;
0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                SIFEEL: 32 IOZEK NOAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTR: USA
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PRECATION DATA:
APPLICATION NUMBER: US/08/451,747
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR DATE: 29-OCT-1993
FILING DATE: 29-OCT-1993
FILING DATE: 29-OCT-1993
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Pred. No. 0.13;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEPHAX: (508) 927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEC ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 96.0
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-451-747-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: un)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111:1111
57 DFMLQGGDF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DFMIQGGDF 9
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METHOD FOR IDENTIFYING ANTI-PARASITIC COMPOUNDS
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       GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASIT
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                        COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
ATTORNEY APAILCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 1;
Pred. No. 0.48;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.08;
                                                                                                                                                            STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELERA: (6(7),523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                              CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: un]
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APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                      DB 2; Length 134; 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 176;
                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34.235
REGISTRATION NUMBER: 34.235
REFERENCE/DOCKET NUMBER: 43.406
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 523-5440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LEMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                     Score 45; DB 2
Pred. No. 0.36;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 1
Pred. No. 0.48;
1; Mismatches
                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08145995A Patent No. 5482850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : Sequence 4, Application US/08145995A
; Patent No. 5482850
                                                                                                     90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 130 WATER STREET
                                                                                             Ouery Match
Best Local Similarity 88.9
Matches 8; Conservative
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 88.9
Matches 8, Conservative
              TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                  1 DFMIQGGDF 9
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                                                 US-08-482-728A-14
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US-08-145-995A-3
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US-08-145-995A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC TITLE OF INVENTION: COMPOUNDS NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                              Score 45; DB 2; Length 176;
Pred. No. 0.48;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45; DB 3;
Pred. No. 0.48;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: RESULCK, DAVID S.
RECISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CARLOW, CLOTILDE K.S. APPLICANT: PAGE, ANTONY
                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09134852
Patent No. 6127148
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617) 523-3400
TELEPAX: (617) 523-6440
TELEX: 200291 STRE UF
INFORMATION FOR SEQ ID NO: 3:
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LENGTH: 176 amino acids
                LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 90.0
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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unknown
SEQUENCE CHARACTERISTICS:
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US-09-134-852-3
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STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109
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                                                                                                              US-08-451-747-4
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32 TOZER ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
UNMERS OF SEQUENCES:
CORRESPONDENCES:
ADDRESSE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/451,747 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 2;
Pred. No. 0.48;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
CLASSIFICATION: 514
ATTORREY AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET WUMBER: NBB-046-DIV
TELECOMMUNICATION INFORMATION:
                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
RECISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEPRAX: (508) 927-1705
                                                     PRIOR APPLICATION DATA
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993
CLASSIFICATION: 514
    APPLICATION NUMBER: US/08/451,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08451747 Patent No. 5821107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: protein
                          FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DFMIQGGDF 9
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REBULT 15

US-09-134-812-4

US-09-134-812-4

US-09-134-812-4

US-09-134-812-4

ERREAT NORDER 4, Application US/09134852

PRICANT: CARLOW, CLOTILDE K.S.

APPLICANT: PAGE, ANTOW

TITLE OF INVENTION: COMPOUNDS

CORRESPONDENCE: 21

ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS 6

ADDRESSEE: CUSHAM

STREET: 130 WATER STREET

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: BOSTON

STATE: MASSACHUSETTS

STREAMCENCE (ANDER: 39-640

TELERAX: (617) 523-340

TELERAY: (617) 523-340

TELERAX: (617) 523-340

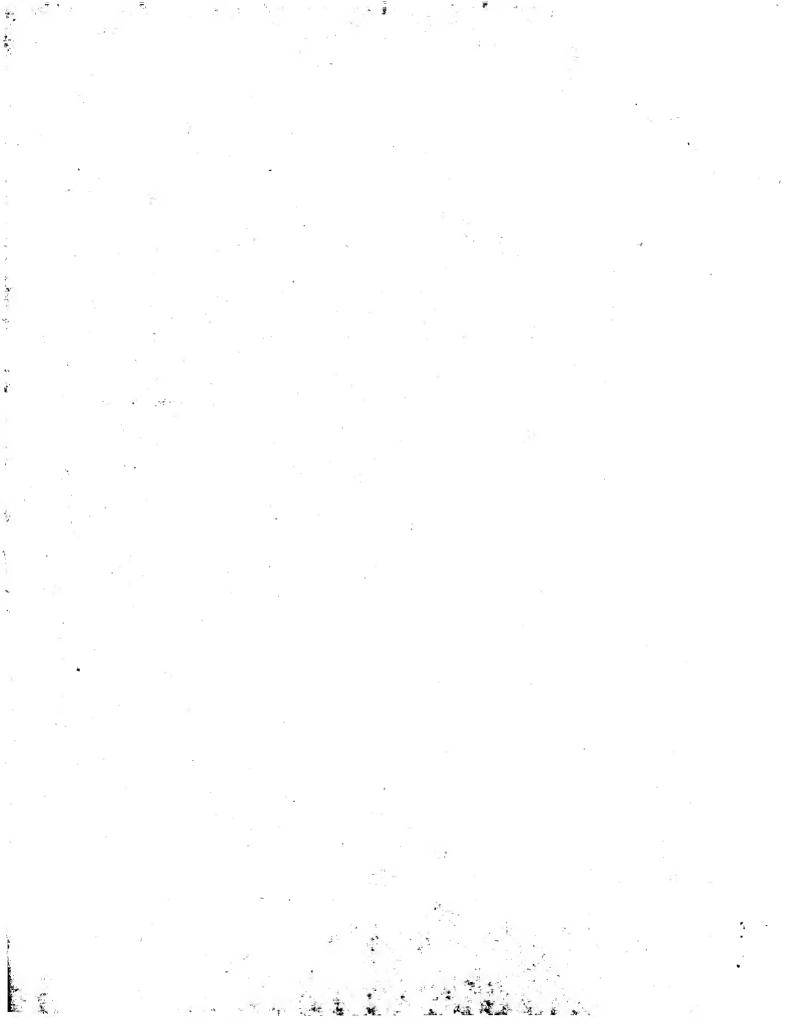
TELERAY: (617) 523-340

TELERAX: (61
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; Gaps 90.0%; Score 45; DB 3; Length 176; 88.9%; Pred. No. 0.48; Live 1; Mismatches 0; Indels Query Match
Best Local Similarity 88.9
Matches 8; Conservative

1 DFMIQGGDF 9

Search completed: January 15, 2002, 13:03:58 Job time: 214 sec



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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 15, 2002, 13:14:58; Search time 24.88 Seconds (without alignments) 13.263 Million cell updates/sec

US-09-720-469-2 50 1 dfwrogopr)9 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	10to d+ +> c)	н		_	~	_	4 homo	mus m	ratt		P34791 arabidopsis		Q06118 streptomyce		P52015 caenorhabdi		P52011 caenorhabdi	_			brugia	P30415 mus musculu	P30414 homo sapien	P25719 saccharomyc	P23285 saccharomyc	P45877 homo sapien	5 trepo	'n	2	Q08752 homo sapien	.1 candi	33	P35627 arabidopsis	60
SOMMAKIES	QI		CYPH_UROFA	CYPB_CAEEL	CYP5_CAEEL	CYPB_CHICK	CYPB_BOVIN	CYPB_HUMAN	CYPB_MOUSE	CYPB_RAT	CYPC_MOUSE	CYP4_ARATH	CYPH_YEAST	PPI_STRCH	CYP2_CAEEL	CYP7_CAEEL	CYP1_CAEEL	CYP3_CAEEL	CYP6_CAEEL	CYPD_YEAST	CYPB_VICFA	CYP1_BRUMA	NKCR_MOUSE	NKCR_HUMAN	CYPC_YEAST	CYPB_YEAST	CYPC_HUMAN	PPIB_TREPA	CYPH_NEUCR	CYP4_BOVIN	CYP4_HUMAN	CYPH_CANAL	CYPH_SCHPO	CYP2_ARATH	CYPH_MAIZE
	DB	1	<del>, -</del>	П	-	<b>-</b>	-	Н	М	_	-	-4	٠,		<b>.</b>	н	-	_	-	н			-	-	<b>⊢</b> ,	→,	-	<b></b>	<b>.</b>	Α.		<b>-</b>		٠, ٠	<b>-</b>
	Length		163	183	204	202	208	208	208	208	212	260	161	165	171	171	192	173	201	225	248	843	1453	1462	182	202	717	215	223	370	370	162	162	169	172
æ	Query Match		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	96.0	96.0	92.0	0.26	92.0	90.0	0.06	0.06	0.06	90.0	90.06	90.0	0.68	0.88	98.0	0.88	0.88	98.0	88.0	84.0	84.0	9.0	0.28
	Score		20	50	20	20	20	20	20	20	20	05.	<b>3</b>	20.0	4.	<b>4</b>	40		45		45	45	45	45	4.4	4.4	4.	4.	4	4	4.	42	7 .	7 -	T &
	Result No.			7	m ·	<b>*</b>	ı,	9	7	<b>30</b> (	σ,	2 .	1.	17	ςŢ.	7,	5 .	91	17	18	5 (	20	21	77	5 6	7 (	7 (	9 10	17	870	5.0	30	31	3.5	33

1 DFMIQGGDF 9

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O9v3g3 drosophila P87051 schizosacch P54985 blattella g P25007 drosophila P34790 arabidopsis O49886 luphnus lut P34887 allium cepa P04374 bos taurus P14851 cricetulus P17742 mus musculu	(PLANTA-INDUCED RUST LES; Uredinlomycetidae;  Les; Uredinlomycetidae;  DF PROTEINS.  DN OF PROLINE IMIDIC SA). CSA MEDIATES SOME N PEIASE LIARITY).  WECTED LEAVES. ALSO (PHASE FORMED) IN VITRO.  PE PPHASE FAMILY.  WECTED LEAVES. ALSO (PHASE PORMED) IN VITRO.  SA) and the EMBL outstation and the EMBL outstation is and the EMBL outstation.  Are no restrictions on its its content is in no way slage by and for commercial its content is in no way slage by and for commercial its content is in no way slage by and for commercial its its content is in no way lasge by and for commercial its its content is in no way lasge by and for commercial its its content is in no way lasge by and for commercial its its content is in no way lasge by and for commercial its its content is in no way lasge by and for commercial its its content is in no way lasge by and for commercial its its content is in no way lasge by and for commercial its its content.	, ra
CYPE_DROME CYP2_COPPO CYP2_COPPO CYPH_BLAGE CYPH_BLAGE CYPH_LOPLU CYPH_LUPLU CYPH_LUPLU CYPH_LUPLU CYPH_LUPLU CYPH_LUPLU CYPH_RATH CYPH_ROYIN CYPH_ROYIN CYPH_RAT ALIGNMENTS	ce update) tion update) SE (EC 5.2.1.8) ING PROTEIN) (PL Urediniomycetes; s. Urediniomycetes; s. THE FOLDING OF P SPORENIZATION ON PP ORY ACTION ON PP SMC (BY SHRILAR A AND RUST-INFEC SPORENIZATION OF P IS PROMERIZATION OF P IS SPORENIZATION OF P IS PRODUCE (BY SHRILAR A AND RUST-INFEC AND RUST-INFEC IN IS PRODUCE IO INFORMATICS AT THE SPORENIZATION OF THE S	No. 0.0064; atches 0;
	in A in a control of the control of	
300 155 1654 172 163 163 163 163	STANDARD; PRT;  9 (Rel. 38, Created)  9 (Rel. 38, Last sequence  9 (Rel. 38, Last sannotat  ROLYL CIS-TRANS ISOMERAS.  ILM) (CYCLOSPORIN A-BINDI  10) (CYCLOSPORIN A-BINDI  10)  10)  11)  12)  12)  12)  13)  14)  15)  16)  16)  17)  18)  18)  18)  18)  18)  18)  18	larity 100.0%; Conservative
882.0 80.00 80.00 880.0 77 80.00 78.00 78.00	ST. (CYVE C.	Similarity 9; Conser
988888877777	Post of the control o	CC
444444WWWWWW	LT 1  CYROPA  CYPROTO  CYPROTO  CYPROTO  CYPROTO  CYPROTO  CYPROTO  CYPROTO  CYPROTO  15-JUL-1999 (Rel. 38, Last sequent  15-JUL-1999 (Rel. 38, Last annota  PEPTIDIX-PROLYL CIS-TRANS ISOMERA  CYCLOPHILIN) (CYCLOSPORIN A-BIND  PROTEIN 28).  Uredinales; Pungi; Basidiomycota;  Uredinales; Punciniaceae; Uromyce  Uredinales; Punciniaceae; Uromyce  NCBL TaxDe-5588;  [1]  SEQUENCE FRON N.A.  STRAIN-IZ; TISSUE-Haustorium;  MEDINE-97249419; PubMed-9150592;  MEDINE-97249419; PubMed-9150592;  MEDINE-97249419; PubMed-9150592;  MEDINE-1Z; TISSUE-Haustorium;  MEDINE-97249419; PubMed-9150592;  MEDINE-1Z; TISSUE-HAUSTORIUM;  PEPTIDE NON A INTIBITY	cal
4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	RESULT  ID AC  CYPH_UROFA  CYPH_UROFA  DE COUGOO  DE FILS-JUL  DE FROTEI  OS NEGLIA  OX NEBLIY  RR HADIA  RR HADIA  RR HADIA  RR HADIA  RR HADIA  CC -!- FU  CC -!- F	Best Lo Matches

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@isb-slb.ch).
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 5 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Caroll P., Rothenfluh A., McGlynn E., Schneider C.,

Caroll P., Rothenfluh A., McGlynn E., Schneider C.,

"S-cyclophilln. New member of the cyclophilin family associated with

"S-cyclophilln. New member of the cyclophilin family associated with

"S-cyclophilln. New member of the cyclophilin family associated with

"S-cyclophilln. New member of the cyclophilin family associated with

"S-cyclophilln. New member of the cyclophilin family

"S-cyclophilln. New member of the cyclophilln."

"S-cyclophilln."

"S-cyclophilln
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15-JUL-1999 (Rel. 38, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
Gallus gallus (Chicken).
Eukaryota: Metazoa: Chordata: Cranlata: Vertebrata: Euteleostom1:
Archosautia: Aves: Neognathae; Galliformes: Phasianidae; Phasianinae;
                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                             Page A.P., Macniven K., Hengartner M.O.; "Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans."; Blochem. J. 317.179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 50; DB 1; Length 204; 100.0%; Pred. No. 0.0081; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isomerase; Rotamase; Multigene family.
SEOUENCE 204 AA: 22366 MW; 22ABB39AD1127BAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfan; PF00160; pro_isomerase; 1.
PR00153; CSAPPIARRASE.
PROSITE: PS00170; CSA_PPIASE_1; 1.
PROSITE: PS00072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
MEDLINE-96276416; PubMed-8694762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002130; CSA_PPIase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
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                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DFMIQGGDF 9
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                                       (CYCLOPHILIN-5).
                                                                                                                                                                                                                      NCB1_TaxID=6239;
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P24367:
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page A.P., Macniven K., Hengarther M.O.; "Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans."; Blochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
1-0CT-1996 (Rel. 34, Last sequence update)
01-0V-1997 (Rel. 35, Last anotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 11 (EC 5.2.1.8) (PPIASE)
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InterPro: IPR00213; CSA_PPIase.
Pries PR00150; pro_isomerase: 1.
PROSITE; PS00170; CSA_PPIASE.1: 1.
PROSITE; PS00770; CSA_PPIASE.1: 1.
ISOMERASE. SECONTS: CSA_PPIASE.2: 1.
ISOMERASE: 1
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(Rel. 34, Last sequence update)
(Rel. 35, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96276416; PubMed=8694762;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ROTAMASE) (CYCLOPHILIN-11).
CYP-11 OR T01B7.4.
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77 DFMIQGGDF 85
                                           57 DEMIQGGDF 65
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01-OCT-1996
01-NOV-1997
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P52013;
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P52018:
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CYP5\_CAEEL

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1.NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last amnotation update)
PEPTIDYL-PROINL GIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl isomerasc with a signal sequence.";
Proc. Natl. Acad. Sci. U.S.A. 88:1903-1907(1991),
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MEDITIPE-91250363; PubMed=2040592;

MEDITIPE-91250363; PubMed=2040592;

Spik G., Haendler B., Delmas O., Mariller C., Chamoux M., Maes P.,

Tartar A., Montreuil J., Stedman K., Kocher H.P., Keller R.,

Hiestand P.C., Movva N.R.;

"A novel secreted cyclophiin-like protein (SCYLP).";

J. Biol. Chem. 266:10735-10738(1991).
                    CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
                                                               ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB. SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Price E.R., 2ydowsky L.D., Jin M., Hunter C.H., McKeon F.D.,
Walsh C.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 50; DB 1; Length 208; Similarity 100.0%; Pred, No. 0.0083; Professoritive 0; Mismatches 0; Indels 9; Conservative 0. Mismatches 0.
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0097C88289AF6276 CRC64;
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MEDLINE-91260697; Pubmed-1710767;
Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 AA.
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MEDLINE-91156714; PubMed-2000394;
                                     PEPTIDE BONDS IN OLIGOPEPTIDES.
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208
208
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22701 MW;
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CYPB HUMAN
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SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY). SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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U-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1995 (Rel. 38, Last annotation update)
PEPTIDYL-PROUTL GIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
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Galat A., Bouet F.;
"Cyclophilin-B is an abundant protein whose conformation is similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutebrila, Cetartiodactyla; Ruminantia, Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
PREVENT SECRETION FROM ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyclosporin: Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
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Bose S., Muecke M., Freedman R.B.;
The characterization of a cyclophilin-type peptidyl prolyl
cis-trans-isomerase from the endoplasmic-reticulum lumen.";
Biochem. J. 300:871-875(1994).
-: FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 50; DB 1; Length 207; 100.0%; Pred. No. 0.0082; Live 0; Mismatches · 0; Indels
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Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D9C0C2E528E25B59 CRC64;
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                                                                                                                                                                                                                                                                                                                   PIR, A40516, A40516.
HSSP, P23284, 1CVN.
InterPro; IPRO02130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PRO0153; CSA_PPIASASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS00172; CSA_PPIASE_1; 1.
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                                                                                                                                                                                                                                                                                            EMBL; M63553; AAA49064.1; -.
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FEBS Lett. 347:31-36(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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TISSUE*Uterus;
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P80311;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schumacher A., Schroeter H., Multhaup G., Nordheim A.; Schumacher A., Schroeter H., Multhaup G., Nordheim A.; Murine cyclophilin-Si: a variant peptidyl-proiyl isomerase with a putative signal sequence expressed in differentiating F9 cells."; Biochim. Biophys. Acta 112:13-22(1991).

-i- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

-i- FUNCTION: PROGRAFINES.

-i- CATALYTIC ACTIVITY: C15-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.

-i- STREELIJIAR LOCATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.

-i- SUBCELIJIAR LOCATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.

-i- SUBCELIJIAR LOCATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
                                                                       01-MAR-1992 (Rel. 21, Last sequence update)
1-UL-1999 (Rel. 38, Last annotation update)
1-PTIUL-1999 (Rel. 38, Last annotation update)
1-PTIUVL-PROLYL CIS-TRANS ISOMERASE B PECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILLN B) (S-CYCLOPHILLN) (SCYLP) (CYP-SI).
                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91260697: Pubmed-1710767;
Hasel K.W. Glass J.R., Godbout M., Sutcliffe J.G.;
"An endoplasmic reticulum-specific cyclophilin.";
Mol. Cell. Biol. 11:3484-3491(1991).
  208 AA.
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InterPro: IPROC02130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; l.
PRINTS; PR00153; CSAPPISMRASE.
                                                 01-MAR-1992 (Rel. 21, Created)
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Best Local Similarity 100.
Matches 9; Conservative
  STANDARD;
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PIR; S21835; S21835.
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SEQUENCE FROM N.A.
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  CYPB_MOUSE
P24369;
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                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION.
MEDLINE-92112948; PubMed-1530944;
Arber S., Krause K.-H., Caronl P.;
"S-cyclophilm is retained intracellularly via a unique COOH-terminal sequence and colocalizes with the calcium storage protein calreticulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                           "Microsequences of 145 proteins recorded in the two-dimensional gel
protein database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).
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108 PREVENT SECRETION FROM ER.
2021 MW; A814481P7EB04579 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 91:5183-5186(1994).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002130; CSA_PPIase.
Pfan, PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSA_PPIASE_1: 1.
PROSITE; PS00170; CSA_PPIASE_1: 1.
PROSITE; PS0072; CSA_PPIASE_2: 1.
Multigene family; 3D_structure.
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-- ENDYMER REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPE.
--- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
--- SIMPLARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPTASE FAMILY.
                                                                                                                            Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.
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100.0%; Score 50; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 9; Conservative 0; Mismatches 0; Indels
endoplasmic reticulum-specific cyclophilin."; Cell. Biol. 11:3484-3491(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
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EMBL; M63573; AAA36601.1; ALT_INIT.
EMBL; M60457; AAA35733.1; -.
                                                                             SEQUENCE OF 64-76 AND 151-157. 
MEDLINE-93162043; PubMed-1286667;
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PIR; A40515; A40515.
PDB; ICYN; 29-JAN-96.
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208 AA;
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91 DFMIQGGDF 99
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            PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
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                                                                                                                           0; Indels
                           PREVENT SECRETION FROM ER
                                         (BY SIMILARITY).
4BBDF5AE40BAD3A7 CRC64;
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BY SIMILARITY
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ID CYPB_RAT
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RESULT 7
CYPB\_MOUSE

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Pfam; PF00160; pro_isomerase;
PRINTS; PR00153; CSAPPISMRASE.
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Best Local Similarity
9, Conserve
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                                        affinity
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01-APR-1993 (Rel. 25, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
  01-MAR-1992 (Rel. 21, Created)
1-MAR-1992 (Rel. 21, Last sequence update)
01-MOV-1995 (Rel. 32, Last annotation update)
PEPTIDEL-PROUKL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAWASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-51).
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MEDLINE-92112948; PubMed-1530944;
Arber S., Krause K.-H., Caroni P.;
"S-cyclophilin is retained intracellularly via a unique COOH-terminal
                                                                                                                                                                             Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                               Iwai N., Inagami T.;
*Molecular cloning of a complementary DNA to rat cyclophilln-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sclurognathi: Muridae: Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence and colocalizes with the calcium storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-90300692; PubMed-2194066;
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MEDLINE-91347379; PubMed-1652374;
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                                                                                                                                                                                                                                                                                                                                                                                                        Kidney Int. 37:1460-1465(1990).
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Matches 9; Conservative
                                                                                                                                                       Rattus norvegicus (Rat).
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PPIC OR CYPC.
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 40. Last annotation update)
PEPTIDYL-PROLYI, CIS-TRANS ISOMERASE, CHLOROPIAST PRECURSOR
(FC. 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBL_TAXID=3702;
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Junan J., Weissman I.L.; cytoplasmic candidates for immunophilin action are revealed by outy for a new cyclophilin; one in the presence and one in the
                                                                                            absence of CsA.";
Cell 66.799-806(1991).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPPPTIDES.
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MEDLINE-98088013; PubMed-9426607;
Chou I.T., Gasser C.S.;
"Characterization of the cyclophilin gene family of Arabidopsis
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                                                                                                                                                                                                                                                                  -:- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.
-:- SUBCELLULAR LOCATION: CYTOPLASMIC.
-:- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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SEQUENCE 212 AA; 22794 MW; C99E7AA5D0FAA04B6 CRC64;
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Pred. No. 0.0085;
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MEDLINE-94179146; PubMed-8132503;
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InterPro; IPR002130; CSA_PPIase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-FDB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last amnotation update)
15-DEC-1998 (Rel. 37, Last amnotation update)
PEPTIDYL-PROVIC CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROPEIN) (CPH) (PPI-1I).
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dietmeier K., Tropschug M.; "Nucleotled sequence of a full-length cDNA coding for cyclophilin (peptidyl-prolyl cistrans isomerase) of Saccharomyces cerevisiae."; Nucleic Acids Ress. 18:373-373(1990).
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-!- SUBCELLULAR LOCATION: CHLOROPLAST STROMA.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
thallana and phylogenetic analysis of known cyclophilin proteins."; Plant Mol. Biol. 35:873-892(1997).
                                                                                                                                                      CHLOROPLAST (POTENTIAL).
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
D412AECBB8A5A3B7 CRC64;
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Cyclosporin; Isomerase; Rotamase; Chloroplast; Transit peptide;
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Pfam: PF00160; pro_isomerase; 1.
PRNTS; PR00150; CSAPISMRASE.
PROSITE; PS00170; CSA_PFIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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SWISS-2DPAGE; P34791; ARATH.
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CYPH_YEAST
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 40, Last annotation update)
PEPTIOPL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAWASE)
(CYCLOPHILIN HOMOLOG).
Streptomyces chrysomallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- ENIXME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                          'Yeast cyclophilin: isolation and characterization of the protein,
                                                                                                                                                                                                                                                             L., Richards C., Harris D., Barrell B.G., Rajandream M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclosporin; isomerase; Rotamase; Multigene family; Acetylation.
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90076969; PubMed-2687115;
Haendler B., Keller R., Hiestand P.C., Kocher H.P., Wegmann G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                Walsh S.V.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACETYLATION.
CE2B71DB8D8C44D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48; DB 1;
Pred, No. 0.016;
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                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION, AND PARTIAL SEQUENCE.
MEDLINE-93160233; Pubmed-8431466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002130; CSA_PP1ase.
Pfam: PF00160; pro_lsomerase: 1.
PRNUTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PP1ASE_1: 1.
PROSITE; PS50072; CSA_PP1ASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17259 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X17505; CAA35545.1; -. EMBL; M30513; AAA34528.1; -. EMBL; Z50046; CAA90376.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.08;
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                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S25443; CSBY.
PIR; S29645; S29645.
                                                                                                                                                            83:39-46(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD; S0002562; CPH1
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Best Local Similarity
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56 DFMLQGGDF 64
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                                                                                                                                           gene.
                                                                                  Movva N.R.;
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Q06118;
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Query Match
Best Local Similarity
Matches 8; Conserv
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STRAIN-BRISTOL N2;
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EFMIQGGDF 74
                                                                                                                                                                                                                                                                                                                                                                                                                        1 DFMIQGGDF 9
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                                                                                                                                                                                         P05092;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 2 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                            Paul A., Uehleh, "Langed 14,7897;
Paul A., Uehleh, "Langed 14,7897;
Paul A., Uehleh, "Sang H., Schlumbohm W., Keller U.;
Part Peromycetes possess peptidy1-prolyl cis-trans isomerases that strongly resemble cyclophilins from eukaryotic organisms.";
Mol. Microbiol. 6:3551-3558(1992).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF TISE SFPECTS VIA AN IMINIBITORY ACTION ON PPIASE.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                     Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page A.P., Macniven K., Hengartner M.O.; "Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans."; Biochem. J. 317:179-185(1996).
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CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n; Isomerase; Rotamase.
165 AA; 17716 MW; 2CF1DF725CD6F47D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 4-41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00160; pro_isomerase; 1
PRNTNS; PR00153; CSAPPISHRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1
PROSITE; PS000770; CSA_PPIASE_2; 1.
                                                                                STRAIN-ATCC 11523;
MEDLINE-93116593; Pubmed-1474897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;
MEDLINE-96276416; PubMed-8694762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, P05092; 3CYS.
InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 215137; CAA78840.1; -.
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Best Local Similarity 88.5،
المالية Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S28020; S28020.
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58 DFMLOGGDF 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclosporin;
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P52010:
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20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 7 (EC 5.2.1.8) (PPIASE) (ROTAWASE)
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Binl L., Held H., Liberatori S., Geier G., Pallini V., Zwilling R.;
Two-dimensional gel electrophoresis of Caenorhabditis elegans
homogenates and identification of protein spots by microsequencing.";
Electrophoresis 18:557-562(1997).
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page A.P., Macniven K., Hengartner M.O.; "Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans."; Biochem. J. 317:179-185(1996).
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-!- CATALVIL CACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPPIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isomerase; Rotamase; Multigene family.
SEQUENCE 171 AA; 18416 MW; 23498E7AA437034C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 1;
Pred. No. 0.041;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro: IPR002130; CSA_PPTase.
Pfam: PF00160; pro_isomerase: 1.
PROSITE: PR00153; CSAPPISMRASE.
PROSITE: PS00170; CSA_PPINSE_1; 1.
PROSITE: PS50072; CSA_PPINSE_1; 1.
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88.9%;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
  Gaps
   Caenorhabditis elegans.
Sukaryota: Metazoa; Nematcoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
  STRAIN=BRISTOL N2;

MEDILINE-96276416; PubMed-8694762;

Page A.P., Macriven K., Hengartner M.O.;

"Cloning and biochemical characterization of the cyclophilin

homologues from the free-living nematode Caenorhabditis elegans.";

Blochem. J. 317:179-185(1996).
  Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PPTASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALVITC ACTIVITY: CIS-TRANK ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
  ..
   92.0%; Score 46; DB 1; Length 171; 88.9%; Pred. No. 0.041; ive 1; Mismatches 0; Indels
   PRT; 192 AA.
   WormPep; Y49A3A.5; CE22213.
InterPro; IPR002130; CSA_PPlase.
   EMBL; U30943; AAC47116.1; -. EMBL; AL033512; CAA22075.1; -HSSP; P05092; 1AWV.
   EMBL; U27559; AAC47125.1;
  Query Match
Best Local Similarity 88.9
Matches 8; Conservative
   STANDARD;
  SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MCMurray A.A.;
  (CYCLOPHILIN-1).
CYP-1 OR Y49A3A.5.
  SEQUENCE FROM N.A.
   66 EFMIQGGDF 74
   1 DFMIQGGDF 9
  NCBI_TaxID=6239;
   CYP1_CAEEL
P52009;
  RESULT 15
CYP1_CAEEL
  ò
  g
```

```
DR Pfam; PF00160; pro_isomerase; 1.
DR PAINTS; PR00153; CSA_PPISMASE_1.
DR PROSITE: PS00170; CSA_PPISME_1: 1.
DR PROSITE: PS00072; CSA_PPISSE_2: 1.
KW Isomerase; Rotannase; Multigene family.
SQ SEQUENCE 192 AA; 20710 MW; C2094D91809ECE85 CRC64;
SQ SEQUENCE 192 AA; 20710 MW; C2094D91809ECE85 CRC64;

Ouery Match
Best Local Similarity 88.9%; Pred. No. 0.047;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps

Qy 1 DFMIQGODF 9
:||||||||
Db 84 EFMIQGODF 92
Search completed: January 15, 2002, 13:14:58
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January 15, 2002, 13:06:15; Search time 42.04 Seconds (without alignments) 16.308 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
   OM protein - protein search, using sw model
   Run on:
```

219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-720-469-2 50 1 DFMIQGGDF 9 Title: Perfect score: Sequence: Scoring table: Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   | peptidylprolyl (so | ٠-    |    |       |       |       | _     | peptidylprolyl iso |       | σ    | , "  | peptidylprolyl iso |      | _    |      | _    |        |      | peptidylprolyl iso |      |      | killer | killer | lprolvl | prolyl |      |      |      | ٠.     | 4 |
|-----------|---------------|--------------------|-------|----|-------|-------|-------|-------|--------------------|-------|------|------|--------------------|------|------|------|------|--------|------|--------------------|------|------|--------|--------|---------|--------|------|------|------|--------|---|
| SUMMARIES | £1            | A5352              | S7154 | T1 | T2158 | A4051 | _     | Æ,    | ⋖;                 |       |      |      |                    |      |      |      |      | S74880 |      |                    |      |      |        |        |         |        |      |      |      | T02489 |   |
|           | Length DB     | 179                |       |    |       |       |       | 212 2 |                    |       |      |      |                    |      |      |      |      |        |      |                    |      |      |        | 507    |         |        |      |      |      |        |   |
| d¢        | Query         | 100.0              | 100.0 |    | 100.0 | 8     | 100.0 | 8     | 100.0              | 100.0 | 98.0 | 96.0 | 0.96               | 0.96 | 92.0 | 92.0 | 92.0 | 90.0   | 0.06 | 0.06               | 0.06 | 0.06 | 0.06   | 0.06   | 88.0    | 88.0   | 88.0 | 88.0 | 88.0 | 88.0   |   |
|           | Score         | 50                 | 20    | 20 | 20    | 20    | 20    | 20    | 50                 | 20    | 49   | 48   | 48                 | 48   | 46   | 46   | 46   | 45     | 45   | 45                 | 45   | 45   | 45     | 45     | 44      | 44     | 44   | 44   | 44   | 44     |   |
|           | Result<br>No. |                    | 7     | m  | ❖     | 'n    | 9     | 7     | <b>30</b> 4        | σ,    | 10   | 11   | 12                 | 13   | 14   | 15   | 16   | 17     | 18   | 19                 | 20   | 21   | 22     | 23     | 24      | 25     | 26   | 27   | 28   | 29     |   |

| peptidylprolyl iso<br>peptidylprolyl iso |                       | Peptidylprolyl 180<br>peptidylprolyl 180<br>estroden recentor- | peptidylprolyl iso | probable peptidyl-<br>probable 40 kd pep | 7,           | peptidylprolyl iso | hypothetical prote |
|------------------------------------------|-----------------------|----------------------------------------------------------------|--------------------|------------------------------------------|--------------|--------------------|--------------------|
| S12324<br>A54204                         | A71261<br>CSNCM       | 749204<br>746579                                               | A45981<br>E86736   | F84808<br>S62327                         | CSZPA        | S22496             | T31517             |
| 77.73                                    | 2 - 2                 | 200                                                            | 00                 | 0 0                                      |              | 00                 | 0                  |
| 205<br>212                               | 223                   | 234                                                            | 370                | 199<br>356                               | 162<br>162   | 169                | 331                |
| 88.0<br>88.0                             | 0.88                  | 0.88                                                           | 88.0               | 86.0<br>86.0                             | 84.0<br>84.0 | 84.0               | 84.0               |
| 4 4<br>4 4                               | 4     4       4     4 | 4 4                                                            | 4 4<br>3           | 4<br>4<br>3                              | 4 4 2 2      | 4 4<br>2 2         | 42                 |
| 30<br>31                                 | 0 0 0<br>7 0 0        | 35                                                             | 37                 | 39<br>40                                 | 477          | <b>4</b> 4         | 4.5                |

# ALIGNMENTS

100.0%; Score 50; DB 2; Length 183; 100.0%; Pred. No. 0.0065;

Query Match Best Local Similarity

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Gaps

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Matches

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A; Molecule type: mRNA
A; Residues: 'MLRLSERN', 1-208 <SPI>
A; Cross-references: GB:M63573; NID:g337998; PIDN:AAA36601.1; PID:g337999
A; Note: the authors' translation begins at an ATG codon in poor context for initiatio
A; Note: parts of this sequence, including the amino end of the mature form, were conf
  C;Species: Homo saplens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Dec-2000
C;Accession: A39118; A39722. A46515. S65742
Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1997, 1991
A;Title: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl iso A;Reference number: A39118; MUID:91156714
   Deptidy prolyl isomerase (EC 5.2.1.8) (S-cyclophilin) precursor - chicken Cispecies: Gallus gallus (chicken) (Cispecies: Gallus gallus (chicken) (Cispecies: Gallus gallus (chicken) (Cispecies: Gallus Gallus (chicken) (Cispecies: Gallus Gallus) (Arguence_revision 28-Feb-1992 *text_change 16-Jul-1999 (Cispecies: As Feb-1992 *sequence_revision 28-Feb-1992 *text_change 16-Jul-1999 (Cispecial) (Arguenity P.) (Arguenity P.) (Arguenity P.) (Arguenity P.) (Arguenity Preliminary (Cispecial) (Arguenity Preliminary)
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A; Rosiduos: 1-208 <HAS>
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A; Cross-references: 6B.M60457; NID:g181249; PIDN:AAA35733.1; PID:g181250
J: Biol. Chem. 266, 10735-10738, 1991
A; Title: A novel secreted cyclophilin-like protein (SCYLP).
A; Reference number: A40515; MUID:91250363
A; Recession: A40515
   peptidylprolyl isomerase (EC 5.2.1.8) B precursor [validated] - human
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A; Cross-references: GBN60857; NID:g181334; PIDN:AAA52150.1; PID:g181335
R; Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
Mol. Cell. Biol. 11, 3484-3491, 1991
A; Title: An endoplasmic reticulum-specific cyclophilin.
A; Reference number: A39722; MuID:91260697
   A)MOLECULE TYPE: MRNA
A)Residues: 1-207 <CAR>
A)Cross-references: GB163553; NID:g212648; PIDN:AAA49064.1; PID:g212649
C)Superfamily: peptidylprolyl isomerase; cyclophilin homology
C)Keywords: cis-trans-isomerase; cyclosporin A binding
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  Indels
   100.0%; Score 50; DB 2; Le
100.0%; Pred. No. 0.0074;
   50; DB 2; LA
No. 0.0073;
matches 0;
   Mismatches
  Score Pred. N
   ..
  100.0%;
   Ouery Match
Best Local Similarity 100.
   Conservative
  Query Match
Best Local Similarity
Matches 9; Conserv
   92
  90 DEMIQGEDE 98
  ō,
   1 DFMIQGGDF 9
  1 DFMIQGGDF
   84 DFMIQGGDF
  RESULT
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   ò
  peptidylprolyl isomerase (EC 5.2.1.8) F31C3.1 [similarity] · Caenorhabditis elegans
   peptidylprolyl isomerase (EC 5.2.1.8) cyp-11 (similarity) - Caenorhabditis elegans N;Contains: cyclophilin
C;Species: Caenorhabditis elegans
  Nicontains: cyclophilin elegans
C: Species: Ceanorhabdits elegans
C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C: Accession: T18978; T24269
R: Page, A.P.; MacNiven, K.
R: Page, MacNiven, K.
R: Page, MacNiven, K.
R: Status: preliminary; translated from GB/EMBL/DDBJ
A: Residues: 1-183 capacian Bristol N2
R: Sims, M.
R: Sims, M.
R: Residues: 219667
A: Reference number: 219667
A: Reference number: 219667
A: Residues: 1-183 capacian Residues: 1
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   Ricottage, A.
submitted to the EMBL Data Library, March 1997
A) Reference number: 219446
A; Reference number: 219446
A; Accession: T21587
A) Status: proliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-204 <WIL>
A; Rosidues: 1-204 <WIL>
A; Residues: 1-204 <WIL>
C; Genetics: Concerned Source: Clone F31C3
   N:Contains: cyclophilin
C:Species: Caenoriabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C;Accession: T21587
  Gaps
Gaps
  ;
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Pred. No. 0.0065;
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A;Introns: 69/3
C;Keyperfamily: peptidy]prolyl isomerase; cyclophilin homology C;Keyperds: cise-trans-isomerase
F;28-190/Domain: cyclophilin homology <CYP>
   A;Map position: 2
A;Introns: 34/3; 148/1
A;Introns: 34/3; 97/3; 148/1
C;Superfamily: peptidylproiyl isomerase; cyclophilin homology C;Seywords: cis-trans-isomerase
F;16-183/Domain: cyclophilin homology <CYP>
Indels
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Mismatches
  100.0%; Sc
100.0%; Pr
tive 0;
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   Ouery Match 100.
Best Local Similarity 100.
Matches 9; Conservative
9; Conservative
   77 DFM1QGGDF 85
   66 DFMIQGGDF 74
   1 DFMIQGGDF 9
  1 DFMIQGGDF 9
  A; Gene: CESP: F31C3.1
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Gaps

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A:Note: sequence extracted from NCBI backbone (NCBIN:73234, NCBIP:73239)
A:Note: parts of this sequence, including the amino end of the mature protein, were c R:Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
Mol. Cell. Biol. 11, 3484-3491, 1991
A;Title: An endoplasmic reticulum-specific cyclophilin.
A;Reference number: A39722; MUID:91260697
   A; MOLecule type: mRNA
A; Residues: 9-216 <NOR>
A; Cross-references: EMBL:X58990; NID:953034; PIDN:CAA41736.1; PID:953035
C; Comment: This protein is distinguished from peptidylprolyl isomerase A by the prese
C; Superfamily: peptidylprolyl isomerase; cyclophilin homology
   C:Keywords: dis-trans-isomerase; cyclosporin A binding; endoplasmic reticulum; T-cell F:1-33/Domain: signal sequence #status predicted <SiG> F:34-216/Product: peptidylproly1 isomerase B #status predicted <MAT> F:43-205/Domain: cyclophilin homology <CYP>
  peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana
N'Alternate names: cyclophilin homolog ROC4; protein F2IF14.200
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 19-May-2000
C.Accession: B53422; T47995
J. Biol. Chem. 269, 7863-7868, 1994
A/Title: Cloning and characterization of chloroplast and cytosolic forms of cyclophil A:Reference number: A53422; MUID:94179146
   A; Molecule type: mRNA
A; Residues: 1-260 <LIP>
A; Cross-references: GB:L14845; NID:9405130; PIDN:AAA20048.1; PID:9405131
R; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; submitted to the Protein Sequence Database, February 2000
  A; Molecule type: mRNA
A; Residues: 9-216 <HAS>
A: Residues: 9-216 <HAS>
R: Cross-references: GB: M60456; NID: g192864; PIDN: AAA37498.1; PID: g192865
R; Nordheim, A.
Submitted to the EMBL Data Library, May 1991
  100.0%; Score 50; DB 2; Length 216; 100.0%; Pred. No. 0.0078;
   C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Reywords: cis-trans-isomerase; cyclosporin A binding F;94-256/Domain: cyclophilin homology <CYP>
  A;Cross·references: EMBL:AL138642
A;Experimental source: cultivar Columbia; BAC clone F21F14
  ..
   A.Map position: 3
A.Intote: 1837; 133/1; 162/3; 181/1; 209/3
A.Note: F21:14.200
  A: Experimental source: teratocarcinoma F9 cells
   0; Mismatches
  9; Conservative
   A; Reference number: S21835
A; Accession: S21835
   A; Reference number: 224481
   A; Molecule type: mRNA
A; Residues: 1-216 <SCH>
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Best Local Similarity
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   A;Status: preliminary
   A;Status: preliminary
   A;Status: preliminary
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   1 DFMIQGGDF
   A: Accession: B39722
   A; Accession: A56861
   A; Accession: T47995
  C; Genetics:
  Q
   õ
R: Mariller, C.; Allain, F.; Kouach, M.; Spik, G.

Biochim. Blophys. Acta 1293, 31-38, 1996

A: Richtle: Studence that human milk isolated cyclophilin B corresponds to a truncated form A: Reference number: S65742; MUID: 96186273

A: Accession: S65742

A: Residues: 26-30:203 cans

A: Residues: 26-203   percent was musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Aberesation: A40047
C; Accession: A40047
C; A40047
C
  A56801
A56801
A56801
A56801
Beptigyprolyl isomerase (EC 5.2.1.8) Cyp-Sl precursor - mouse
Briternate names: cyclophilin B: cyclophilin-Sl; cyclosporin A-binding protein
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A56801; B39722; S21835
C;Accession: A56801; B39722; S21835
C;Accession: A56801; B39722; J3182, 1991
Biochim: Biophys: Acta 1129, 13-22, 1991
A;Title: Murine cyclophilin-Sl: a variant peptidyl-prolyl isomerase with a putative sign
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   Gaps
   Gaps
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   Length 208;
   Length 212;
   0; Indels
  peptidylprolyl isomerase (EC 5.2.1.8) (cyclophilin C) - mouse
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Pred. No. 0.0075;
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   Pred. No. 0.(
Mismatches
   100.0%; Score 50; 100.0%; Pred. No.
  ;
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  Ouery Match
Best Local Similarity 100.
Matches 9; Conservative
  Ouery Match
Best Local Similarity 100.،
9; Conservative
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   1 DFMIQGGDF 9
   1 DFMIQGGDF 9
   91 DFMIQGGDF
  ò
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   g
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Gaps

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Indels

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Paptidylprolyl isomerase (EC 5.2.1.8) - Streptomyces chrysomallus
N;Alternate names: cyclophilin A; cyclosporin A-binding protein
C;Species: Streptomyces chrysomallus
C;Species: Streptomyces chrysomallus
C;Accession: S28020: S25676
C;Accession: S28020: S25676
R;Pahl, A.: Uchlein, M.; Bang, H.; Schlumbohm, W.; Keller, U.
MOI. Microbiol. 6, 3551-3558, 1992
A;Fitle: Streptomycetcs possess peptidyl-prolyl cis-trans isomerases that strongly re
A;Fitle: Streptomycetcs possess paptidyl-prolyl cis-trans isomerases that strongly re
   A; Molecule types DNA
A; Residues: 1-162 cMUR>
A; Residues: 1-162 cMUR>
A; Cross-references: EMBL: Z50046; NID: 9899393; PIDN: CAA90376.1; PID: 9899403; GSPDB: GNO
A; Experimental source: strain A8972
B; Hasumi, H.; Nishikawa, T.
Biochim. Biophys. Acta 1161, 161-167, 1993
A; Title: Purification and properties of multiple molecular forms of yeast peptidyl pr
A; Reference number: S29645; MUID: 93160233
A; Accession: S29645
  A.Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds A.Description: catalyzes the cis-trans isomerization of peptidylproline griffinity fo C.Superfamily: peptidylprolyl isomerase; cyclophilin homology C.Reywords: acetylated amino end; blocked amino end; cis-trans-isomerase; cyclophilin homology C.Reywords: acetylated amino end; cis-trans-isomerase; cyclosporin F:1-162/Domain: cyclophilin homology CXPP.
F:2-162/Product: peptidylprolyl isomerase, cytosolic #status experimental cMATP F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
  peptidylprolyl isomerase (EC 5.2.1.8) a, cytosolic - fungus (Fusarium sporotrichioide
   N.Alternate names: cyclophilin A
C:Species: Fusarium sporotrichioides
C:Species: 3-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 19-Jan-2001
C;Accession: JTG686; PNO166; JTG702
R:Chow, L.P.: Ueno, Y.; Tsuglta, A.
submitted to JIPID, June 1995
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   Gaps
  A,Cross-references: EMBL:215137; NID:946835; PIDN:CAA78840.1; PID:946836
C,Superfamily: peptidylproly1 isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase; cyclosporin A binding
F;2-165/Domain: cyclophilin homology <CYP>
  .;
0
   ö
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   Length 162;
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   0; Indels
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A; Residues: 'X',3-8,'X',10;30-37;75-78;81-85;159-162 <HAS>
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88.9%;
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   57 DFMLQCGDF
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A; Accession: S57980
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   C; Genetics:
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  Matches
   RESULT
   RESULT
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  qq
  ô
   qq
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   peptidylprolyl isomerase (EC 5.2.1.8), cytosolic - yeast (Saccharomyces cerevisiae)
Nalternate names: cyclophilin A; cyclosoprin A-binding protein; peptidylprolyl isomeras
C; Species: Saccharomyces cerevisiae
C; Species: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 05-Nov-1999
C; Accession: S23443; JQ0125; S57980; S29645
R; Diermeier, K.; Tropschug, M.
Nucleic, Acids Res. 18, 373, 199
A; Title: Nucleotide sequence of a full-length cDNA coding for cyclophilin (peptidyl-prol
   Ayaccesion: 323443

A;Molecule type: mRNA

A;Roldues: 1-162 colbs.

A;Roldues: 1-162 colbs.

A;Roldues: 1-162 colbs.

B;Haendler, B.; Keller, R.; Hiestand, P.C.; Kocher, H.P.; Wegmann, G.; Movva, N.R.

Gene B3, 39-46, 1989

A;Title: Yeast cyclophilin: isolation and characterization of the protein, cDNA and gene

A;Reference number: J00125; MUID:90076969
  A:Experimental source: thymus A:November 1995 A:Note: submitted to the EMBL Data Library, November 1995 C;Comment: This protein contains a cyclophilin-related domain, two 140K nuclear phosphop splicing by binding to splicing factors containing serine-arginine repeats protein.
   ;
  0
  A; MOLECULE type: mRNA
A;Residues: 1-754 <NES>
A;Cross-references: EMBL:U40763; NID:g1117967; PIDN:AAB40347.1; PID:g1117968
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: JG5314; G02262
R;Nestel, F.P.; Colwill, K.; Harper, S.: Pawson, T.; Anderson, S.K.
R;Nestel, F.P.; Colwill, K.; Harper, G.: Pawson, T.; Anderson, S.K.
A;Title: RS Cyclophilins: Identification of an NK-TRI-related cyclophilin.
A;Reference number: JG5314; MUID:97128820
  Gaps
  Gaps
  A; Cross-references: GB:M30513; NID:g171313; PIDN:AAA34528.1; PID:g171314
A; Note: part of this sequence was confirmed by protein sequencing
R; Murphy, L.; Richards, C.; Harris, D.
submitted to the EMBL Data-Library, July 1995
A; Reference number: S57971
   CDC28/cdc2-like kinase associating arginine-serine cyclophilin - human
   ..
  ö
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Conservative
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Best Local Similarity 100.
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A;Gene: GDB:CYP; CARS-CYP
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Best Local Similarity
Matches 8; Conserv
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  150 DFMIQGGDF 158
   71 DFMVQGGDF 79
   6
  1 DFMIQGGDF 9
   1 DFMIOGGDF
   A; Accession: JC5314
  RESULT
   g
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peptidylprolyl isomerase (BC 5.2.1.8) 2K520.5 (similarity) - Caenorhabditis elegans X.Contains: cyclophilin C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000 R.Steward, C. R.Steward, C. submitted to the EMBL Data Library, March 1997
  A; Cross.references: EMBL: Z92822; PIDN: CAB07303.1; GSPDB: GN00021; CESP: ZK520.5
   A, Map position: 3
A, Introns: 23/3; 107/3
A, Introns: 23/3; 107/3
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F;3-171/Domain: cyclophilin homology <CYP>
  0; Indels
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  Score 46; DB 2;
Pred. No. 0.041;
L; Mismatches
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Job time: 226 sec
   A.Experimental source: clone ZK520 C;Genetics:
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88.9%;
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A; Accession: T27882
   A; Molecule type: DNA
A; Residues: 1-172 <WIL>
  66 EFMIQGGDF 74
  74
   1 DFMIQGGDF 9
  A; Gene: CESP: ZK520.5
  :11111111
66 EFMIQGGDF
  RESULT
  a
   οy
  qq
   Peptidylprolyl isomerase (EC 5.2.1.8) Y75B12B.2 [similarity] - Caenorhabditis elegans N;Contains: cyclophilin Cipecials caenorhabditis elegans C;Species: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000 R;White, S. S. White, S. S. Submitted to the EMBL Data Library, October 1998 A;Reserve number: 220360 A;Recession: T27371 A;Residues: 220360 A;Residues: 1-171 - CWIL.> A;Cross-references: EMBL:AL032663; PIDN:CAA21760.1; GSPDB:GN00023; CESP:Y75B12B.2 A;Residues: 23/3, 107/3 A;Map position: 5107/3 C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Reywords: cis-trans-isomerase F;3-171/Domain: cyclophilin homology 
A:Description: Amino acid sequence of peptidyl-prolyl isomerase a from Fusarium sporotril
A:Reference number: JT0686
A:Mocession: JT0686
A:Molecule type: protein
A:Residues: 1-179 ccH0>
A:Residues: 1-179 ccH0>
A:Residues: 1-179 ccH0>
A:Residues: 1-179 ccH0>
A:Reference number: Pw0160
A:Reference number: Pw0160
A:Residues: 1-41 ccH0>
A:Residue
  Superfamily: peptidylprolyl isomeraes; cyclophilin homology (Skywords: cis-trans-isomeraes; cyclophilin homology cycwords: cis-trans-isomeraes; cyclophilin homology cycwords: cis-trans-isomeraes; cyclosporin A binding; cytosol; nucleotide binding; p-1 F:179/Domain: cyclophilin homology cycyb (CYP) F:59-6/Toomain: cyclophilin homology cycyb (CYP) F:59-6/Toomain: peptidylprolyl isomeraes specific cPPI> F:59-6/Toomain: peptidylprolyl isomeraes specific cPPI> F:51-72/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted F:23/Binding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted F:13/Binding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted F:13/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted F:13/Psinding site: phosphate (Thr) #status predicted F:172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted F:172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted F:172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted F:172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted F:172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted F:172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted F:172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted F:172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted F:172/Binding site: phosphate (Thr) #status predicted F:172/Binding #
  A. Reference number: JT0702
A. Reference number: JT0702
A. Reference number: JT0702
A. Reference number: JT0702
A. Reference number: JT0702
A. Residues: 1-179
C. Comment: This enzyme catalyzes interconversion of the cis and trans imino peptide bond C. Superfamily: peptidylproly! isomerase: cyclophilin homology
C. Rewords: cis-trans-isomerase: cyclosporin A binding; cytosol; nucleotide binding; p-1
F.1-179/Domain: cyclophilin homology <CXP.
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   Gaps
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   Score 48; DB 2; Length 179;
Pred. No. 0.016;
1; Mismatches 0; Indels
  DB 2; Length 171;
   0; Indels
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Best Local Similarity 88.9%;
Matches 8; Conservative
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70 DFMLQGGDF 78
  1 DFMIQGGDF 9
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Gaps ;

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January 15, 2002, 13:05:27; Search time 81.32 Seconds (without alignments) 8.198 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
  Total number of hits satisfying chosen parameters:
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   SUMMARIES
  OM protein · protein search, using sw model
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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51
   A_Geneseq_1101:*
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  Title:
Perfect score:
Sequence:
   Scoring table:
   Database :
  Searched:
   Run on:
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|           |   |        | Description     |   | Human evelophilin | Hillman secreted pro | Human Secretary pro | Human Cyclopalin | Human cvclonhilin | Distriction of the country | numan cancer assoc | Human colon cancer | Unimpo DOM opposed | וותוומוו במן פווכסתפת | Human cvclophilin | Himman Cucloud | annual Creation in the state of | Atanianbsis challa | Arabidopsis thalia |
|-----------|---|--------|-----------------|---|-------------------|----------------------|---------------------|------------------|-------------------|----------------------------|--------------------|--------------------|--------------------|-----------------------|-------------------|----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------|--------------------|
| COLUMNICO |   |        | 1D              |   | AAY 59923         | AAG00090             | AAB73302            | *^^ / 000        | AAB73301          | AAB43878                   |                    | AAG75931           | AAM24287           |                       | AAY 59924         | AAU01197       | AACO5073                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | COCOCA             | AAG05072           |
|           |   |        | DB              |   | 77                | 21                   | 22                  | 1                | 22                | 7                          | 1 6                | 77                 | 22                 | 1 6                   | 7,                | 22             | 7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 1                  | 2                  |
|           |   |        | Match Length DB | • | ν.                | 166                  | 211                 | 1                | 216               | .291                       |                    | 717                | 8                  | : :                   | 7                 | 207            | 254                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 1                  | 259                |
|           | æ | Query  | Match           |   | 7007              | 100.0                | 100 0               |                  | 100.0             | 100.0                      |                    | 87.4               | 78.4               | 3.0                   | 0.0               | 76.5           | 76 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                    | 76.5               |
|           |   |        | Score           |   | 7.0               | 51                   | 51                  | 1                | 7                 | 51                         | •                  | 7 6                | 40                 | 20                    | 2                 | 39             | 39                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 1                  | 20                 |
|           |   | Result | No.             | - | -                 | 7                    | ~                   | , -              | 4                 | 'n                         | 9                  | ٥                  | 7                  | a                     | 0                 | σ              | 10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ,                  | 7                  |

Tumour antigen peptides derived from cyclophilin B for treatment and diagnosis of tumours  $\,$ 

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Claim 4; Page 50; 64pp; Japanese.

|      | 12          | 30           | 76.5         | 4224                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 0       | A A LAS A 23 S | March 2 F.O.           |
|------|-------------|--------------|--------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------|----------------|------------------------|
|      | 13          | 38           | 74.5         | 114                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 22      | AAB64737       | Human secreted ord     |
|      | 14          | 38           | 74.5         | 315                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 10      | AAP90099       | in TA of               |
|      | 15          | 38           | 74.5         | 315                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 13      | AAR27483       |                        |
|      | 16          | 38           | 74.5         | 326                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 11      | AAR06037       | A oute                 |
|      | 17          | 37           | 72.5         | 108                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 21      | AAG03830       | secreted               |
|      | 18          | 37           | 72.5         | 108                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 22      | AAM20480       | de #6914 e             |
|      | 2,0         | ر د<br>د د   | U. 2.        | 108                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 22      | AAM35140       | Peptide #9177 enco     |
|      | 2.0         | , "          | , c          | 1 1 4<br>1 4 5<br>1 4 5<br>1 7 5 | 7 (     | AAB54 / 35     | Gene 14 human secr     |
|      | 22          | 37           | 72.5         | 145                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 1 4     | AAR72917       | Porcine peptidyl-p     |
|      | 23          | 37           | 72.5         | 145                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 9       | AAR72961       | Porcine peptidy; p     |
|      | 24          | 37           | 72.5         | 163                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 17      | AAR13726       | Boyine Cyclophilin     |
|      | 25          | 37           | 72.5         | 164                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 10      | AAP90431       | Cyclophilin Homo       |
|      | 26          | 37           | 72.5         | 165                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 19      | AAW56028       | Calcineurin protei     |
|      | 27          | 37           | 72.5         | 165                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 5       | AAG03831       | Human secreted ord     |
|      | 28          | 37           | 72.5         | 165                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 22      | AAU01195       | Human cyclophilin      |
|      | 29          | 36           | 70.6         | 72                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 22      | AAB59512       | Human secreted pro     |
|      | 30          | 36           | 70.6         | 141                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 13      | AAW44367       | Breast cancer-asso     |
|      | 31          | 36           | 70.6         | 141                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 55      | AAB98719       | Breast cancer-asso     |
|      | 32          | 36           | 20.6         | 276                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 21      | AAY52295       | Human isomerase ho     |
|      | 33          | 36           | 20.6         | 296                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 22      | AAB98722       | Human breast cance     |
|      | 34          | 36           | 70.6         | 301                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 21      | AAB51902       | Gene 22 human secr     |
|      | 35          | 36           | 20.6         | 301                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 51      | AAB51903 ·     | Human secreted pro     |
|      | 36          | 91           | 20.6         | 301                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 22      | AAB98721       | Human breast cance     |
|      | 3.7         | 36           | 70.6         | 494                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 20      | AAY34531       | Porphorymonas ging     |
|      | 38          | 36           | 20.6         | 532                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 20      | AAY34398       | Porphorymonas ging     |
|      | ο e         | 36           | 70.6         | 782                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 50      | AAY42283       | Salmonella dublin      |
|      | 0 4         | 35           | 9.89         | 212                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 21      | AAY92048       | A. niger peptidyl-     |
|      | 4.1         | ω i          | 2.99         | 152                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 7.0     | AAW77504       | o .                    |
|      | 2 0         | ₩ (          | 66.7         | 212                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 7       | AAR32353       | Cyclophilin C. Mu      |
|      | 7           | n (          | 00           | 309                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 91      | AAR70762       | Meningococcal grou     |
|      | 4. c        | 7) r         | 66.7         | 309                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 8 6     | AAW21741       | Neisseria meningit     |
|      | 2           | <b>*</b>     | . 00         | ς <b>Τ</b> ς                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | β       | AAW 21 / 4 4   | sseria menin           |
|      |             |              |              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         | ALIGNMENTS     |                        |
|      |             |              |              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |                |                        |
| A.   | RESILT. 1   |              |              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |                |                        |
| AA   | 53          |              |              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |                |                        |
| Ω    | AAY6992     | m            | standard;    | l; peptide;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | de;     | 9 AA.          |                        |
| XX   |             |              |              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |                |                        |
| AC . | AAY69923    | 123;         |              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |                |                        |
| ¥ 6  | 11          | 0            | ,            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |                |                        |
| XX   | 11-AFR-2000 | 0007-3       | (rirst       | st entry)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | £       |                |                        |
| DE   | Human       | cyclophilin  | ohilin       | B peptide                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ide     | fragment #3.   |                        |
| XX   |             | •            |              | ŧ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 3       |                |                        |
| ×    |             | hilin        | B; hu        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | tumour  |                | cytotoxic T-cell; CTL; |
| Ϋ́   | HLA an      | antigen      | ; diag       | agnosis;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | tumour; | thera          |                        |
| X    | ;           |              |              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |                |                        |
| SOX  | НОШО        | Homo sapiens | ,<br>m       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |                |                        |
| PN   | M09967      | W09967288-A1 | _;           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |                |                        |
| X 6  | 20-00       | 1000         |              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |                |                        |
| Z X  | ת           | - DEC - 1999 |              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |                |                        |
| PF   | 24 - JUN    | -JUN-1999    | 66 :         | 99WO-JP03360                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 360.    |                |                        |
| PR A | 25-JUN      | -JUN-1998;   | 86 :         | 98JP-017844                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 449.    |                |                        |
| X    |             |              |              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |                |                        |
| PA P | (SUMU)      |              | TOMO<br>T.K. | SUMITOMO PHARM CO<br>ITOH K.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | O LTD   | ۵.             |                        |
| ***  |             |              |              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |                |                        |

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  Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
   The present sequence is a polypeptide encoded by one of a large number of 5 EST9 derived from mRNAs encoding secreted proteins. The 5' EST9 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such EST9 are not well suited for isolating cDNA sequences have been obtained those cases where longer cDNA sequences have been obtained in those cases where longer cDNA sequences have been obtained, the full 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' EST9 are also used in diagnostic, foremsic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
             This sequence represents a cyclophilin B peptide of the invention. The
                              peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
   Gaps
   ;
   100.0%; Score 51; DB 21; Length 9; 100.0%; Pred. No. 4.3e+05;
   Indels
   ö
   Duclert A, Giordano J;
   Claim 13; SEQ ID 4171; 71pp + CD-ROM; English.
   Mismatches
  Human secreted protein, SEQ ID NO: 4171.
  AAG00090 standard; Protein; 166 AA.
   0;
   21-FEB-2000; 2000EP-0200610.
   99US-0122487
  (first entry)
   Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
  Dumas Milne Edwards J,
  WPI; 2000-500381/45.
N-PSDB; AAC00096.
   1 gfgyknskf 9
   1 GFGYKNSKF 9
  9 AA;
   (GEST ) GENSET.
   Homo saplens.
   EP1033401-A2.
   26-FEB-1999;
  06-OCT-2000
   06-SEP-2000,
   Sequence
  AAG00090;
  Sequence
   AAG00090
  g
X 2 2 2 2 2 X 2 3
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51; DB 21; Length 166; No. 0.076;

Score Pred.

100.0%;

Query Match Best Local Similarity

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The invention relates to a composition for modulating somatolactogenic function, comprising oyclophilin B (GypB), a mutant of cyclophilin B (articularly a CypB mutant in which residues 2-12 of the mature protein care absent) or an inhibitor of the interaction of cyclophilin B with a somatolactogenic formone; The invention along the set of a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB levels in a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic function in the animal, and cyclophilin B mutant or a composition comprising of cyclophilin B is useful in the treatment of somatolactogenic function in the animal. A composition comprising cyclophilin B is useful in the treatment of impublication comprising cyclophilin B with a somatolactogenic formone, is useful for treating mutant or a composition comprising cyclophilin B mutant or a composition comprising cyclophilin B mutant or a composition comprising cyclophilin B with a somatolactogenic formone, is useful for treating HIV infection, breast and prostate cancer, glganism/acromegaly, and hyperprolactinaemia. The present sequence represents a human cyclophilin B creaminal mutant, CybB-AIAKE.

Sequence represents a human cyclophilin in the specification, but seed form the wild-type CybB sequence shown on pages 17-18.
   Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone \,
  Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature; muscle wastling; osteoporosis; HIV infection; breast cancer; prostate cancer; gigantian; acromegaly; hyperprolactinaemia; c-terminal deletion mutant; muteln.
  Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.
   Length 211;
  Score 51; DB 22;
Pred. No. 0.096;
   AAB73302 standard; protein; 211 AA.
   Disclosure; Page -; 21pp; English.
  100.0%;
   10-AUG-2000; 2000WO-US21789.
  22-MAY-2001 (first entry)
  (UYPE-) UNIV PENNSYLVANIA.
  Clevenger CV, Rycyzyn MA;
   WPI; 2001-211249/21.
   Best Local Similarity
  211 AA;
   W0200113113-A1.
Homo sapiens.
   19-AUG-1999;
  22-FEB-2001
   AAB73302;
  Sequence
   Query Match
             85
  AAB73302
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AAB43878 standard; Protein; 291

AAB43878

AAB43878;

93

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function, comprising cyclophilin B (CypB), a mutant of cyclophilin B (pypB), a method for cyclophilin B with a season; or an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, protacting growth hormone). The invention also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic formone, and a method for functions using CypB and a somatolactogenic formone, and a method for diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB levels in a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic function in the animal, and cyclophilin B with a somatolactogenic hormone, is useful for inhibiting somatolactogenic function in the animal. A composition of cyclophilin B with a somatolactogenic hormone, is useful for treatment of a composition of composition of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprise composition comprise composition comprise composition composition comprise composition comprise composition         0
  Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone
   The invention relates to a composition for modulating somatolactogenic
  Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteoporosis; HIV infection; breast cancer;
        Gaps
   gigantism/acromegaly, and hyperprolactinaemia. The present a represents human cyclophilin B.
     ;
0
   prostate cancer; gigantism; acromegaly; hyperprolactinaemia,
     Indels
     ő
     Mismatches
   AAB73301 standard; protein; 216 AA.
   Claim 1; Page 17-18; 21pp; English.
  ·,
  99US-0149752.
   10-AUG-2000; 2000WO-US21789.
  Human cyclophillin B (CypB).
  (first entry)
  Clevenger CV, Rycyzyn MA;
   (UYPE-) UNIV PENNSYLVANIA.
9; Conservative
   WPI; 2001-211249/21
  85 gfgyknskf 93
  1 GFGYKNSKF 9
  WO200113113-A1.
   Homo sapiens.
  22-MAY-2001
   19-AUG-1999;
   22-FEB-2001.
   AAB73301:
  sedneuce
   Sequence
  4
Matches
   AAB73301
  RESULT
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dermatological; neuroprotective; cardiant; thrombolytic; coaquiant; micropic; vasotropic; antipsoriatic and antiangiogenic. The nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate haemostatic or thrombolytic activity, modulate haemostatic or disorders, neurological disease and
  AAC78449 to
   bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
  Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antinheumatic; antiasthmatic; antiasthmatic; antiallergic antibacterial; candiant; dermaclogical; neuroprotective; thrombolytic; coaquiant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; altergic reaction; graft versus host disease; organ rejection; neurological disease; drug screening.
  AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
  include: cytostatic; proliferative; vulnerary; immunomodulator;
antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
  Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer - \,
   Human cancer associated protein sequence SEQ ID NO:1323.
   Claim 11; Page 1974-1975; 2352pp; English.
  (HUMA-) HUMAN GENOME SCI INC.
  08-MAR-2000; 2000WO-US05882.
   08-FEB-2001 (first entry)
   the present invention.
   Rosen CA, Ruben SM;
  2000-587533/55.
  291 AA;
   N-PSDB; AAC78087
   W0200055350-A1.
   Homo sapiens.
  12-MAR-1999;
   21-SEP-2000.
   Sequence
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Gaps

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100.0%; Score 51; DB 22; Length 216; 100.0%; Pred. No. 0.099; Indels ()

Query Match 100.

Best Local Similarity 100.

Matches 9; Conservative

AAG75931

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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensis, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
   Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
  Human; sheep; plg; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; dlagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
   DB 22; Length 83; 3.7;
  Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Cao Y, Drmanac RA, Zhang J, Werhman T;
  Mismatches
  Claim 20; Page 1183-1184; 1275pp; English.
  Human EST encoded protein SEQ ID NO: 1812.
   Score 40;
Pred. No.
  AAY69924 standard; peptide; 11 AA.
  AAM24287 standard; Protein; 83 AA
   78.4.
100.08; Pre-
   78.4%;
  2000US-0491404.
2000US-0617746.
   03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
   25-JAN-2001; 2001WO-US02687
   11-APR-2000 (first entry)
   (first entry)
  protein of the invention.
  Conservative
  WPI; 2001-476164/51
  Query Match
Best Local Similarity
Matches 7; Conserv
               94 gygykgskf 102
   (HYSE-) HYSEQ INC.
   83 AA;
   N-PSDB; AAH98946
  ||||||||
77 gfgykns 83
  WO200154477-A2.
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  25-JAN-2000;
17-JUL-2000;
   12-OCT-2001
   02-AUG-2001
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  AAM24287;
   Sequence
  AAY69924

1D AAY6

XX

AC AAY6

XX

DT 11-AI
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AAM24287
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  AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens. The colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P caperession. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P Dy expressing in a patient's genome that affect the activity of P Dy expressing cancering the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
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                                    ö
  Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
   Gaps
                                    Gaps
   present invention.

18. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
   colon cancer; colon cancer antigen; diagnosis; detection;
   ö
                                    ;
0
  Score 42; DB 22; Length 112;
Pred. No. 2.2;
1; Mismatches 1; Indels
                                    Indels
   Human colon cancer antigen protein SEQ ID NO:6695.
                                    .;
                   Pred. No. 0.13;
Mismatches
   Rosen CA;
  Claim 11; Page 8161-8163; 9803pp; English.
  AAG75931 standard, Protein, 112 AA.
100.08; Pic
   Birse CE,
  (HUMA-) HUMAN GENOME SCI INC.
  Query Match 82.4%;
Best Local Similarity 77.8%;
Matches 7; Conservative
   28-SEP-2000; 2000WO-US26524.
  99US-0157137.
  (first entry)
                   Best Local Similarity 100.
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   colorectal carcinoma,
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  112 AA;
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   1 GFGYKNSKF 9
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  WO200122920-A2.
  Homo sapiens.
  29-SEP-1999;
03-NOV-1999;
  03-SEP-2001
   05-APR-2001
   Ruben SM,
   AAG75931;
  Sequence
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mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperprolliferative disorders e.g. cancer, and deafness.
   The present sequence represents human cyclophilin D which is a mitochondrial core component. Cyclophilins interact with other mitochondrial core components e.g. adenine nucleotide translocator (ANT) proteins to requilate MPT. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial poir component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between
   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
  New nucleic acid expression constructs, useful for screening for agents
   mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered
   that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule
   Score 39; DB 22; Length 207;
Pred. No. 14;
Mismatches 2; Indels
  Arabidopsis thaliana protein fragment SEQ ID NO: 1339.
  AAG05073 standard; Protein; 254 AA.
   Disclosure; Fig 8; 186pp; English.
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  990S-0123180.
990S-0123548.
990S-0125788.
990S-0126264.
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77.8%;
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99US-0128234.
  99US-0121825
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   Best Local Similarity 77.8
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  Arabidopsis thaliana
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   207 AA;
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   87 gfgykgstf
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05-MAR-1999;
09-MAR-1999;
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29-MAR-1999;
01-APR-1999;
06-APR-1999;
   06-SEP-2000.
   23-MAR-1999
   Sequence
  AAG05073;
   Query Match
  RESULT 10
   AAG05073
            NAME OF THE PROPERTY OF THE PR
   Db
  δλ
  6
  This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
   Human; adenine nucleotide translocator; ANT; MTP; cyclophilin D; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
  Gaps
   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy.
   Tumour antigen peptides derived from cyclophilin B for treatment and
  0;
  Wiley SE, Andreyev AY, Frigeri LG;
  76.5%; Score 39; DB 21; Length 11; 100.0%; Pred. No. 0.73; 1ve 0; Mismatches 0; Indels
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   Claim 4; Page 50; 64pp; Japanese.
  (SUMU ) SUMITOMO PHARM CO LID
   99WO-JP03360,
   98JP-0178449.
  Human cyclophilin D protein.
   03-NOV-2000; 2000WO-US30535
   99US-0434354
  (first entry)
  Best Local Similarity 100.
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   Murphy AN, Clevenger W,
Velicelebi G, Davis RE;
  diagnosis of tumours
   WPI; 2000-116932/10.
  11 AA;
  Gomi S;
   (MITO-) MITOKOR.
  (ITOH/) ITOH K.
  3 GYKNSKF 9
  ||||||||
| gyknskf 7
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   24-JUN-1999;
  25-JUN-1998;
   29-DEC-1999
   07-SEP-2001
   10-MAY-2001
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                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection and therapy of cervical cancer - using specific cervical cancer-associated proteins as targets for treatment or as indicators for detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cervical cancer-associated protein; CvC; tryptic peptide; human; detection; treatment; Nup358; nucleoporin; non-chromatin protein.
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                                                                                                                                                                                                                                             21; Length 259;
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17;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                 AAW54235 standard; peptide; 3224 AA.
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990S-0160980.
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990S-0161404.
990S-0161405.
990S-0161359.
990S-0161359.
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                                                                                                                                                                                 99US-0161920
99US-0161992
                                                                                                                                                                                                         99US-0161993
99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keesee SK, Obar R, Wu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                 10-AUG-1998 (first entry)
                                                                                                                                                                                                                                                          Best_Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MATR-) MATRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Nup358 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-230271/20
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                                                                                                                                                                                                                                                                                             1 GFGYKNSKF 9
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                                                                                                         25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-1998.
                                 21-OCT-1999;
21-OCT-1999;
                                                          21-OCT-1999;
22-OCT-1999;
                                                                                  22-OCT-1999;
                                                                                                                                                                      26-0CT-1999;
28-0CT-1999;
                                                                                             22-0CT-1999
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                                                                                                                                                                                                         28-OCT-1999
29-OCT-1999
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                                                                                                                                                                                                                                               Query Match
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The polynucleotide sequences given in AAF33037 to AAF33085 encode the human secreted proteins given in AAB64666 to AAB64714. AAB64715 to AAB64771 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues are expressed in Examples of activities include: Cytostatic, antitheumatic; antithrhitic; dermalogical; cardiant; antihifiammatory; gastrointestinal; and anti-ulcer. The polynucleotides and polypeptides can be used in the prevention, treatment and diagnosis of diseases associated with inappropriate polypeptide expression. Disorders that may be treated or prevented include solid tumours, rheumatoid arthritis, psoriasis, diabetic retinopathy, myocardial angiogenesis, Crohn's disease and ulcers. The polynucleotides and their complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and therefore which patients may be in need of restorative therapy. The polypeptides
                                                                                                                                                                                                  ó
cervical cancer cell than in a normal human cervical cell, as determined by 2D-get alectrophoresis. The methods can be used for the early and rapid detection of cervical cancer, for treating cervical cancers and for monitoring the efficacy of such treatment.
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; diagnosis; cytostatic; antirheumatic; antiarthatic; dermalogical; cardiant; antiinflammatory; anti-ulcer; gastrointestinal; solid tumour; rhemmatoid arthritis; psoriasis; diabetic retinopathy; myocardial anglogenesis; Croin's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding 49 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases such as tumors, rheumatoid arthritis, psoriasis and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein sequence encoded by gene 14 SEQ ID NO:131,
                                                                                                                                                                                                  ..
0
                                                                                                                                                        Length 3224;
                                                                                                                                Score 39; DB 19; Length 32. Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 500-501; 520pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Komatsoulis GA;
                                                                                                                                                                                                                                                                                                                                                                   AAB64737 standard; Protein; 114 AA.
                                                                                                                                                      76.5%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2000; 2000WO-US14928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0138633
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                   Query Match 76.5
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                         3105 gfgfknsif 3113
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                                                                                               3224 AA
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                                                                                               Sequence
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may also be used as antigens in the production of antibodies against the polypeptide and in assays to identify modulators (agonists and antiagonists) of polypeptide expression and activity. The anti-polypeptide antibodies and antiagonists may also be used to down regulate expression and activity. AAR33036 to AAR53036 and AAR64665 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria gonorrhoeae Protein 1 gene sequences
sed for detection of N. gonorrhoea infection and
producing vaccines for prevention or treatment of infection
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                                                                                                                                                                                                                                                                                                                                                           Neisseria gonorrhoea (NG); NG strain FA19; peptide sequence;
                                                                                                                          DB 22; Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide sequence of Protein IA of Neisseria gonorrhoea (NG) strain FA19. Used in prepn. of vaccines for prevention or treatment of NG infection. The region is a signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 10; Length 315;
Pred. No. 32;
0; Mismatches 2; Indels
                                                                                                                                                   1; Indels
                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYNC ) THE UNIVERSITY OF NORTH CAROLINA
                                                                                                                          Score 38;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                    Protein IA of N. gonorrhoea strain FA19.
                                                                                                                                                                                                                                                                                                                                                                                                                                     1..18
/label- signal-peptide
                                                                                                                                                                                                                                                               315 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; fig 3; 70pp; English.
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77.8%;
                                                                                                                          74.58;
77.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88WO-US04225.
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                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 77.0.
                                                                                                                                                   7; Conservative
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                                                                                                                                      Best Local Similarity
                                                                                    114 AA;
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| 173 gfnyknsgf 181
                                                                                                                                                                                                 26 gfgyksscf 34
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                                                                                                                                                                                                                                                                                                            01-NON-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                          Protein IA
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                                                                                     Sequence
                                                                                                                        Query Match
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The sequence given is encoded by the protein IA gene of Neisseria gonorrhoeae. PIA is a major outer membrane proteins of N. gonorrhoeae which act as a porin. Porins are believed to act in cells by channelling low molecular weight substances across the hydrophobic lipid outer membrane. Elucidation of the gene sequences of PIA and PIB allows the production of antigenic fragments by recombinant DNA techniques. These fragments can be used as immunogens in vaccine compositions for the prevention of gonorrhoea, and also on immunoassays for diagnosis of infection. See also AAR27484.
                                                                                                                                        Protein IB; PIB; Neisseria gonorrhoeae; PIA; outer membrane; porin; hydrophobic; lipid; outer membrane; antigen; immunogen; vaccine; gonorrhoea; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fragments of Neisseria Gonorrhoeae protein IA or IB - used as vaccines for preventing gonorrhoeal infection, and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 315; 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.5%; Score 38; DB
77.8%; Pred. No. 32;
tive 0; Mismatches
                                                                                                                                                                                                                                       1..18
/label= Signal_peptide
19.315
/label= Mature_protein
                                                                                                                                                                                                                         Location/Qualifiers
                            AAR27483 standard; Protein; 315 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 3; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                92WO-US02006.
                                                                                                                                                                                                                                                                                                                                                                                           91US-0669492
                                                                                                                                                                                                                                                                                                                                                                                                                       (UYNC-) UNIV NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sparling FP;
                                                                                   (first entry)
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N-PSDB; AAQ29138.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carbonetti N,
                                                                                                                                                                                                                                                                                                                                                                13-MAR-1992;
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                                                                                                                                                                                                                                                                                                           W09216223-A.
                                                                                   08-MAR-1993
                                                                                                                                                                                                                                                                                                                                      01-0CT-1992.
                                                                                                                Protein IA
                                                                                                                                                                                                Synthetic
                                                      AAR27483;
                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                    Protein
RESULT 15
AAR27483
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Gaps

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Indels

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Best Local Similarity 77.8 Matches 7; Conservative

Query Match

|| |||| | 173 gfnyknsgf 181 1 GFGYKNSKF 9

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Search completed: January 15, 2002, 13:05:27 Job time: 198 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                              OM protein - protein search, using sw model
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Run on:

January 15, 2002, 13:03:58; Search time 37.64 Seconds (Without alignments) 5.381 Million cell updates/sec

US-09-720-469-3 51 Title: Perfect score: Sequence:

1 GFGYKNSKF 9 Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

212252 Total number of hits satisfying chosen parameters: 212252 seqs, 22503292 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_AA:\* Database :

/cgn2\_6/ptodata/2/jaa/5A\_COMB.pep:\*
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/cgn2\_6/ptodata/2/jaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/2/jaa/PCTUS\_COMB.pep:\* 5. .. ..

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	Sequence 10, Appl	7. 4	13.	Sequence 13, Appl	13.		8,	Sequence 9, Appli	ď	6	12,	Sequence 34, Appl	34.	15,	G	ω,	Ξ	8	1,	8,	11,	14,	14.	Α.	20,	18	5, A
	ID	US-08-482-728A-10	US-08-142-897-7	US-08-145-995A-13	US-08-451-747-13	-09 - 13	US-08-482-728A-11	US-08-142-897-8		-80	US-09-134-852-9	US-08-482-728A-12	-08	US-08-989-045-34	US-08-482-728A-15	US-08-482-728A-9	US-08-145-995A-8	US-08-145-995A-11	US-08-451-747-8	US-08-451-747-11	US-09-134-852-8	US-09-134-852-11	US-08-658-639-14	US-08-944-604-14	US-08-989-386-3	US-08-944-604-20	US-08-944-604-18	US-08-142-897-5
	DB	N	~	_	7	m	~	-4		~	<b>(</b> ~)	2	N	m	a	α	-	-	~	~	m	m	7	4	ď	4	4	7
	Length	126	208	161	161	161	126	163	164	164	164	126	3224	3224	126	127	165	165	165	165	165	165	141	141	276	296	301	212
Ouerv	Match	100.0	100.0	88.2	88.2	88.2	82.4	78.4	78.4	78.4	78.4	76.5	76.5	76.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	9.02	9.02	9.02		9.02	
	Score	51	51	45	45	45	42	40	40	40	40	.6E	39	39	37	37	37	37	37	37	37	37	36	36	36	36	36	34
Result	S.	п	7	m	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27

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Gaps 0;

Query Match
100.0%; Score 51; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels

1 GFGYKNSKF 9

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sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 16, Appli Sequence 16, Appli Sequence 14, Appli Sequence 14, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 6, Appli	
US-08-096-182A-2 US-08-877-109-2 PCT-08-798-756-2 US-08-798-756-2 US-08-142-728A-16 US-08-145-95-14 US-08-145-95-14 US-08-451-747-14 US-08-451-747-14 US-08-459-351-19 US-08-459-351-19 US-08-459-351-19 US-08-459-351-19 US-08-459-351-6 US-08-459-351-6 US-08-459-351-6 US-08-459-351-6 US-08-459-351-6 US-08-460-533-6	ALIGNMENTS  T. 1 1-482-728A-10 uence 10, Application US/08482728A nut No. 5968802 NBEAL INFORMATION: APPLICANT: Wang, Bruce APPLICANT: Bisher, Joseph APPLICANT: Bayan, Donald TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin COMPRESSEE: Flehr, Hobbach, Test, Albritton ADDRESSEE: Flehr, Hobbach, Test, Albritton ADDRESSEE: Flehr, Hobbach, Test, Albritton COMPRESSEE: APPLOR STATE: California COUNTRY: United States SITY: San Francisco STATE: California COUNTRY: United States SIP: 94111-4187 COMPUTER READBLE FORM: MADIUM TYPE: Ploppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SUSTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: 38,304 RECISTRATION NUMBER: 38,304 RECISTRATION NUMBER: 38,304 RECISTRATION NUMBER: 38,304 RECISTRATION NUMBER: A-61230/DJB/RMS TELERAX: (415) 398-3249 TELERAX: (415) 781-1989 TELERAX: (415) 781-1889
3009 3009 3009 3009 3009 3009 300 300 30	ALI  8-482-728A-10  8-482-728A-10  8-482-728A-10  4DEREAL INFORMATION:  APPLICANT: Wang, Bruce APPLICANT: Payan, Donald ADDRESSEE: Flehr, Hobbach, Test COUNTRY: San Francisco STATE: California ZIP: 94111-4187 COMPUTER READABLE FORM: WADDITYPE: FOUR FORDER: 1008/482,7 FLING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/482,7 FLING DATE: Of JUN-1995 CLASSIFICANTON UNMBER: 38,304 REFERENCE/DOCKET NUMBER: 38,304 REFERENCE/DOCKET NUMBER: 38,304 TELECHMUNICATION INFORMATION: TELECHMUNICATION INFORMATION: TELECHMUNICATION INFORMATION: TELECHMUNICATION INFORMATION: TELECHMUNICATION INFORMATION: TELECHMUNICATION OF SEC ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 126 amino acids TYPE: protein MOLECULE TYPE: protein
666.7.7.7.666.7.7.666.7.7.7.666.7.7.7.666.7.7.7.666.7.7.7.666.7.7.7.666.7.7.7.7.666.7.7.7.7.666.7.7.7.7.7.666.7.7.7.7.7.7.666.7	A-10  Ti Application U FORMATION TI Fisher, Jos TI Fisher, Jos TI FAMPINATION TI FISHER, JOS TI PAYAN, DONA TINVENTION: NO TINCATION: NO TI
**************************************	ULT 1  08-482-728A-10  atent No. 5968802  GENERAL INFORMATION: APPLICANT: Wang, Bruce APPLICANT: Wang, Bruce APPLICANT: Payan, Donal TITLE OF INVENTION: No. NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: Flehr, Hoh COMPUTER: California COMPUTER: EADABLE FORM: MEDIUM TYPE: Flehry COMPUTER: 1BM PC COMP OPERATING SYSTEM: PC- SOFTWAME: 1BM PC COMP OPERATING SYSTEM: PC- SOFTWAME: 1DM TYPE: O7-UNY- FLLENTH: SILVE ROBIN M. REGISTRATION NUMBER: URCSISTRATION NUMBER: TELECOMMUNICATION INFORM TELECOMMUNICATION
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	RESULT 1 US-08-482-7 Sequence Patent NO GENERAL APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC COMPUT COM

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ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC. STREET: 32 TOZER ROAD CITY: BEVERLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: CARLOW, CLOFILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN
                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILIGO DATE: 29-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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Pred. No. (
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PRIOR APPLICATION NOWBER: US 08/145,995
FILING DATE: 29-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/08451747 Patent No. 5821107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-0CT-1993
N: 514
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88.9%;
                                            130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 86.5.
مع 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS: unknown
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MOLECULE TYPE: protein US-08-145-995A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MASSACHUSETTS
COUNTRY: USA
                                                                             STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                               BOSTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 01915
                                                                                                                           02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-451-747-13
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                                                                                                                    Sequence 7, Application US/08142897
Patent No. 5447852
GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: DUIN, TRACY D.
REGISTRATION NUMBER: 34,587
REFERCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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77 GFGYKNSKF 85
    28 GFGYKNSKF 36
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                                                                                                                                                                                                                                                                                                                                                                                                            94105
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                                                                                   RESULT 2
US-08-142-897-7
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GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
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                                                                            Score 45; DB 3; Length 161;
Pred. No. 0.27;
); Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 5968802el Nuclear Cyclophilin
21
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILIG DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fiehr, Hobbach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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L; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/08482728A; Patent No. 5968802
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: Sequence 8, Application US/08142897
; Patent No. 5447852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNE/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION TELEPHONE: (415) 781-1989 TELEPRAX: (415) 398-3249 TELEX: 910 277299 INFORMATION FOR SEQ ID NO: 11:
                                                                            88.2%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Fisher, Joseph
TITLE OF INVENTION: No. 596
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 amino acids
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                                                                      Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-482-728A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California COUNTRY: United
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28 GYGYKGSKF 36
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                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-08-482-728A-11
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Patent No. 6127148
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 161;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 2
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                            NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY PREDICTION OF THE CONTRACT OF THE CONTRACT OF THE COMMUNICATION INPORMATION TELEPHONE: (617) 523-3400
TELEPHONE: (617) 523-3400
TELEFAX: (617
                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 161 amino acids TYPE: amino acid STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.2%;
88.9%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.9%,
Braa 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 130 WATER STREET CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-451-747-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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42 GFGYKGSKF 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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STREET: 32 TOZER ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
29-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                       Score 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESINCK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 9, Application US/08451747
; Patent No. 5821107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: NE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
                                                                                                                                                                     TELEPHONE: (617) 523-3400
TELEPAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                         78.48;
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SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                               164 amino acids
                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 77.8
Matches 7; Conservative
             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   unknown
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STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-145-995A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GFGYKNSKF 9
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                                                   FILING DATE:
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US-08-451-747-9
                                                                                                                                                                                                                                                                 LENGTH:
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Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                  NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/142,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 1
Pred. No. 2.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                 PLINE CATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
PILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
PLINE DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy, D.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELEPHONE: 415-326-2420
TELEPHONE: 415-326-2420
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                     and Uses
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.48;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 130 WATER STREET
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-142-897-8
                                                                                                         CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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STATE: MASSAC
                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                            COUNTRY:
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1 GFGYKNSKF 9
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US-08-705-660-34
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APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANYONY
APPLICANT: PAGE, ANYONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: CUSHMAN
STREET: 130 WATER STREET
                                                                                                                                                                                                                                           DB 2; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.4%; Score 40; DB 3; Length 164; 77.8%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                             Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
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Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                         0; Mismatches
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APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
ATTORNEY/AGBNT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6127148
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TELEFAX: (617) 523-6440
TELEA: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                           78.48;
77.88;
                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
STRANDEDNESS: unknown
                                      TOPOLOGY: unknown
HOLECULE TYPE: protein
US-08-451-747-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                    11111 | |
45 GFGYKGSSF 53
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                             1 GFGYKNSKF 9
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STATE:
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Parent No. 5685683
GENERAL INFORMATION:
APPLICANT: OBAR, ROBERT
APPLICANT: OBAR, ROBERT
APPLICANT: OBAR, ROBERT
TITLE OF INVENTION: DETECTION OF CERVICAL CANCER
NUMBER OF INVENTION: DETECTION OF CERVICAL CANCER
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                             No. 5968802el Nuclear Cyclophilin
21
                                                                                                                                                                             ADDRESSEE: Flehr, Hobbach, Test, Albritton
ADDRESSEE: Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
CITY: San Francisco
CITY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPRRATING SYSTEM: PC-DOSS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A-61230/DJB/RMS
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/482,728A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
Sequence 12, Application US/08482728A Patent No. 5968802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989 TELEX: 910 277299 INFORMATION FOR SEQ ID NO: 12:
                                     GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTON: No. 596
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.58;
77.88;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.5
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-482-728A-12
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28 GFCYKGSTF 36
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Gaps
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                                                                             Length 3224;
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Pred. No. 6.2;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
APPLICANT: Payan, Donald
TITLE OF INVENTION: NO. 5968B02el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton
ADDRESSEE: 6 Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIL RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLEASTFICATION: 435
ATTORNEY/ACENT INPORMATION:
NAME: SILVa, RODIN M.
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 398-2349
TELEPHONE: (415) 398-2349
TELEPHONE: (415) 398-2349
INFORMATION FOR SEQ ID NO: 15:
SEGURENCE CHARACTERISTICS:
'ENGTH: 126 amino acids
                                                                               DB 3;
                                                                                                                    1; Mismatches
                                                                               Score 39;
                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                        ; Sequence 15, Application US/08482728A
; Patent No. 5968802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08482728A patent No. 5968802
                                                                             76.5%;
                                                           Query Match
Best Local Similarity 77.0v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States 21P: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) MOLECULE TYPE: protein US-08-482-728A-15
, MOLECULE TYPE: peptide US-08-989-045-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Wang, 1
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                                                                                                                                                         1 GFGYKNSKF 9
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                                                                                                                                                                                                                                                       RESULT 14
US-08-482-728A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KEESEE, SUSAN
APPLICANT: KEESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WING-JYE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: DETECTION OF CERVICAL CANCER
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: INDEPT OF COMPATIBLE COMPUTER: INDEPT COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/989,045 FILING DATE: CLASSIFCATION: ATTORNEY ACCEST.
                                        SOFTWARE: Patentin Release #1.0, version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,660 FILLING DATE:
                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GREENHALGH, DUNCAN A
RECISTRATION NUMBER: 38 678
REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
TELECOMMUNICATION INFORMATION:
TELEFRONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 34:
SEGUENCE CHARACTERISTICS:
LENGTH: 3224 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: GREENHALGH, DUNCAN A
REGISTRATION NUMBER: 38,678
REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 246-7000
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39;
Pred. No. 6
          IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/08989045 Patent No. 6027905
                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.5%;
77.8%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Florm:
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
        COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                       linear
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3105 GFGFKNSIF 3113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: linear
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STREET: Lac
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-989-045-34
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APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
ITTLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: 6 Herbert
STREEPET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
IPT SAN FRANCISCO
STATE: APLIA187
COMPUTER REABBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
STILIG DATE: 07-JUN-1995
CLASSIFICATION: NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELEPHONE: (415) 398-3249
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
TELEFAX: 910 277299
TELEFAX: 10 277299
TELEFAX: UNKNOWN
MOLECULE TYPE: EMOTION
TOPOLOGY: UNKNOWN

WOLECULE TYPE: PIFOTE PROTEIN
US-08-482-728A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

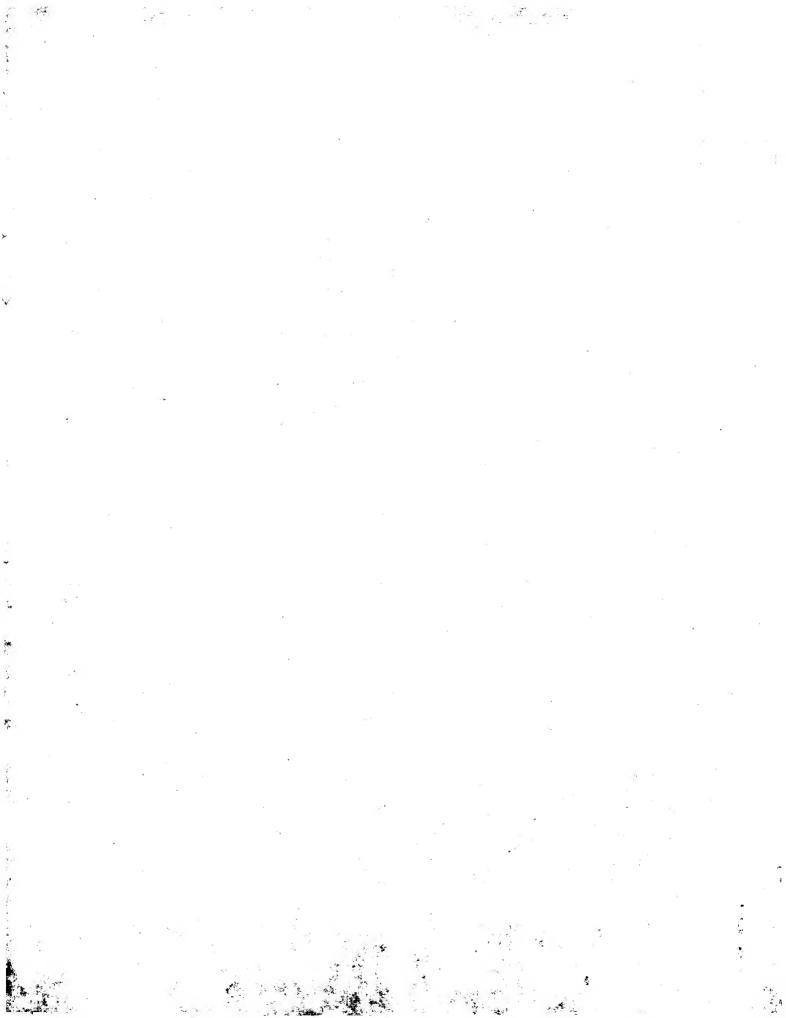
Query Match

12.5%; Score 37; DB 2; Length 127;
Best Local Similarity 77.8%; Pred. No. 6.2;

Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GFGYKNSKF 9
|||||| | 1
28 GFGYKGSCF 36
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Search completed: January 15, 2002, 13:03:59 Job time: 215 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                               OM protein - protein search, using sw model
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January 15, 2002, 13:06:15; Search time 42.04 Seconds (Without alignments) 16:308 Million cell updates/sec US-09-720-469-3 51 1 GFGYKNSKF 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0,5 Scoring table:

219241 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:\* pir2:\* pir3:\* pir4:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	T.	osi [vlord] best idv] brolvi iso						_	_	_	_	_				5	0		embra	lectin-like adhesi	peptidylprolyl iso	_	_			_			hypothetical profe	DNA-directed DNA p
		S71547	CSHUB	A56861	A45000	863995	A54204	A40516	A56814	CSHYAC	CSMSA	CSRTA	JT0686	CSNCM	S68767	A41581	S58884	S24202	A39951	PC4425	CSCK	CSBOAB	CSPGA	CSHUA	B38388	S51497	571849	S66681	A70422	JC7381
	Query Match Length DB	183 2				164 2				164 1	164 1	164 1	179 2	·		207 2		308 2		330 2	162 1	163 1		165 1					330 2	•
æ	Query Match	100.0	100.0	100.0	88.2	82.4	82.4	80.4	78.4	78.4	78.4	78.4	78.4	78.4	76.5	76.5	76.5	74.5	74.5	74.5	72.5	72.5	72.5	72.5	72.5	9.07	20.6	0	70.6	
	Score	51	51	51	45	42	42	41	40	40	40	40	40	40	39	39	39	38	38	38	37	37	37	37	37	36	36	36	36	36
	Result No.	-4	2	m	4	S	9	7	œ ·	on :	10	11	13	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	2-hydroxymuconate-	2-hydroxymuconate-	probable ribose/oa	proline tRNA liga	hypothetical prote	penicillin-binding	genome polyprotein	phosphoglycerate m	hypothetical prote	peptidylprolyl iso	peptidylprolyl iso	-	outer membrane pro	nembrane	membrane
T21487	T31275	JC5419	D70184	686890	F72393	JH0438	JQ1895	H81387	D82882	S28020	A40047	S25509	S25508	S25507	S25506
2	~	-	П	N	N	~	-	7	~	~	2	~	7	7	7
795	283	286	536	616	707	864	3163	492	121	165	212	293	294	295	295
70.6	68.6	68.6	68.6	9.89	9.89	68.6	9.89	67.6	66.7	66.7	66.7	66.7	66.7	66.7	66.7
36	35	35	35	35	35	35	35	34.5	34	34	34	34	34	34	34
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4 5

## ALIGNMENTS

л 1	Peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K - rat N:Alternate names: cyclophilin B; PPIASE C;Species: Rattus norvegicus (Norway rat) C;Date: 15-Nov-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999	R. Ruecknagel, 1134 Feifer, T.; Rahfeld, J.U.; Schaerfke, M.; Fischer, G. submitted to the Protein Sequence Database, November 1996 A; Reference number: S71547	Ariaciecules type: protein Ariaciecules: 1-183 ARUS- Ariaciecules: 1-183 ARUS- Ariaciecules: 1 iver Ariaciecules: 1 iver ariaciecules:	F;1-183/Product: peptidylprolyl isomerase, isoform 20.3K #status experimental <mat> F;10-172/Domain: cyclophilin homology <cyp></cyp></mat>	Ouery Match 100.0%; Score 51; DB 2; Length 183; Best Local Similarity 100.0%; Pred. No. 0.022; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 GFGYKNSKF 9	52 GFGYKNSKF 60
RESULT 1	S71547 peptidylprol N;Alternate C;Species: E C;Date: 15-N	R; Ruecknagel submitted to A; Reference A; Accession	A; MOIECUIE A; Residues: A; Experiment C; Superfamil C; Keywords;	F;10-172/Don	Query Matc Best Local Matches	0y 1 GF	Db 52 GE

# RESULT

Peptidylprolyl isomerase (EC 5.2.1.8) B precursor (validated) - human NiAtternate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin C;Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 08-Dec-2000 C;Accession: A39118; A39722. A40515; S65742 Proc. Natl. Accession: A39118; A39722. A40515; S65742 Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907, 1991 A71tle: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl iso A;Reference number: A39118; MuID:91156714

A; Molecule type: mRNA
A; Residues: 1-208 <PRI>
A; Cross-references: GB:M60857; NID:g181334; PIDN:AAA52150.1; PID:g181335
A; Cross-references: GB:M60857; NID:g181334; PIDN:AAA52150.1; PID:g181335
B; Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
Mol. Cell. Biol. 11, 3184-3491, 1991
A; Title: An endoplasmic reticulum-specific cyclophilin.
A; Reference number: A39722; MUID:91260697
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: MRNA
A; Residues: 1-208 CHAS>
A; Cross-references: GB:M60457; NID:g181249; PIDN:AAA35733.1; PID:g181250

Gaps

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Indels

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R;Martinez-Gonzalez, J.; Hegardt, F.G.
Eur. J. Biochem. 234, 284-292, 1995
A;Title: Characterization of a cDNA encoding a cytosolic peptidylprolyl cis-trans-iso
A;Reference number: S63995; MUID:96096751
A;Reference number: S63995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Lightowlers, M.W.; Haralambous, A.; Rickard, M.D. Mol. Biochem. Parasitol. 36, 287-289, 1989
A;Title: Amino acid sequence homology between cyclophilin and a cDNA-cloned antigen o A;Reference number: A45000; MUID:90014983
                                                  A; Molecule type: mRNA
A; Residues: 9-216 <NOR>
A; Cross-references: BMBL:X58990; NID:953034; PIDN:CAA41736.1; PID:953035
A; Cross-references: EMBL:X58990; NID:953034; PIDN:CAA41736.1; PID:953035
C; Comment: This protein is distinguished from peptidylprolyl isomerase A by the prese
C; Superfamily: peptidylprolyl isomerase; cyclophilin homology
C; Keywords: cis-trans-isomerase; cyclosporin A binding; endoplasmic reticulum; T-cell
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-216/Product: peptidylprolyl isomerase B #status predicted <MAT>
F:43-205/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptidylprolyl isomerase (EC 5.2.1.8) [similarity] - tapeworm (Echinococcus granulosu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-164 <MAR>
A;Cross-references: EMBL:X87418; NID:91235942; PIDN:CAA60869.1; PID:91772496
C;Superfamily: peptidylptoroly1 isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase
F;3-164/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.Contains: cyclophilin
C.Species: Echinococcus granulosus
C.Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 08-Sep-2000
C.Accession: Ad 5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:J04664; NID:g158843; PIDN:AAA29056.1; PID:g158844 C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Reywords: cis-trans-isomerase cyclophilin homology C;Reywords: cis-trans-isomerase cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 51; DB 2; Length 216; 100.0%; Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptidylprolyl isomerase (EC 5.2.1.8) - German cockroach
NiAlternate names: cyclophilin
C.Species: Blattella yermanica (German cockroach)
C.Species: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
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Best Local Similarity
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A; Residues: 1-161 <LIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 GFGYKNSKF
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A; Recession: 565742

A; Recession: 565742

A; Recession: 565742

A; Recession: 565742

A; Recession: 565742

A; Residues: 26.30;203 **AMRA

A; Reperimental source: milk

C; Comment: This protein is distinguished from peptidylprolyl isomerase A by the presence C; Cenemic: This protein binds to and is inhibited by the immunosuppressive drug cyclosper C; Genetics:
A; Gene: GDB:PPIB

A; Gene: GDB:PPIB

A; Gene: GDB:PPIB

A; Cross-references: GDB:127610; OMIM:123841

A; Map position: 15q21-15q22

C; Function: artalyzes the cis-trans isomerization of peptidylproline peptide bonds C; Superfamily: peptidylprolyl isomerase; cyclophilin homology

C; Keywords: cis-trans-isomerase; cyclosporin A binding; glycoprotein; T-cell

F; A; Domain: signal sequence #status predicted <S.C.

F; Rec-203/Froduct: peptidylprolyl isomerase B #status experimental <MAT>

F; 35-197/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ascession: Anset: Asset: Asset
R:Spik, G.; Haendler, B.; Delmas, O.; Mariller, C.; Chamoux, M.; Maes, P.; Tartar, A.; M. J. Biol. Chem. 266, 10735-10738, 1991
A:Pitler A novel secreted cyclophilin-like protein (SCYLP).
A:Reference number: A40515; MUD:91250363
A:Rocession: A40515
A:Rocession: A70515
A:Rocession: A40515
A:Rocession: A405
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C; Species: Mus musculus (house mouse)
C; Accession: A56861; B39725; S21835
R; Schumacher, A.; Schroter, H.; Multhaup, G.; Nordheim, A.
Biochim: Biophys. Acta 1129, 13-22, 1991
A; Title: Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a putative sign A; Reference number: A56861; MUD:92096454
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F:140/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 0.025;
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A;Reference number: S21835
A;Accpssion: S21835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
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Best Local Similarity 100...
9, Conservative
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A; Residues: 9-216 <HAS>
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Gaps

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Length 161; 1; Indels #text\_change 20-Jun-2000

Length 164;

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Peptidylprolyl isomerase (EC 5.2.1.8) [similarity] - mouse (fragments)
N.Alternate names: cyclophilin homolog SIP24
C.Species: Was musculus (house mouse)
C.Species: Was musculus (house mouse)
C.Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 02-Sep-2000
C.Accession: A56814
R.Davis, T.R.; Tabatabat, L.; Bruns, K.; Hamilton, R.T.; Nilsen-Hamilton, M.
Biochim. Biophys. Acta 1095, 145-152, 1991
A;Title: Basic fibroblast growth factor induces 3T3 fibroblasts to synthesize and sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds C;Superfamily: peptidylproly isomerase; cyclophilin homology C;Reywords: cis-trans-isomerase; cyclosporin A binding; T-cell F;3-164/Domain: cyclophilin homology <CYP.
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NA Alternate names: cyclophilin A; cyclosporin A-binding protein A
C; Species: Mus musculus (house mouse)
C; Species: Mus rusculus (house mouse)
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C; Accession: 510327; S66416; S40742
R; Hasel, R.W.; Sutcliffe, J.G.
Nucleic Acids Res. 18, 4019, 1990
A; Title: Nucleotide sequence of a cDNA coding for mouse cyclophilin.
A; Reference number: 510327; MuID:90326555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Experimental Source: BALB/c 3T3 cells
A:Note: sequence modified after extraction from NCBI backbone
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 38;
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Pred. No. 2.4;
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Pred. No. 0.54;
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Best Local Similarity 77.8;
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A; Residues: 1-38 < DAV>
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Best Local Similarity
Matches 7; Conserv
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C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 28 Feb-1992 #sequence_revision 28 Feb-1992 #text_change 16-Jul-1999
C; Accession: A40516
R; Caroni, P.; Rothenfluh, A.; McGlynn, E.; Schneider, C.
J; Biol. Chem. 266, 10739-10742, 1991
A; Title: S-cyclophilin. New member of the cyclophilin family associated with the secretch A; Reference number: A40516; MUID:91250364
A; Accession: A40516
A; Accession: A40516
A; Residues: 1-207 ccAR>
A; Molecule type: mRNA
A; Residues: 1-207 ccAR>
A; Coss references: GB:M63553; NID:9212648; PIDN:AAA49064.1; PID:9212649
C; Reywords: cis-trans-isomerase; cyclophilin homology
C; Reywords: cis-trans-isomerase; cyclosporin A binding
                                                                                                                                                                                                                                                                                                                                                                                                                   Concession: A54204
Rischeider, H.; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zurini, M.G.; Quesniau Blochemistry 31, 81318-8124, 1994
A: Title: Human cyclophilin C: primary structure, tissue distribution, and determination A: Reference number: A54204; MUID:94304830
A: Reference number: A54204, MUID:94304830
A: Reference number: A54204, MUID:94304830
A: Residues: 1-212 colls
A: Residues: Calls
A: R
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                                       Indels
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C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Kgywords: cis-trans-isomerase; cyclosporin A binding
F;37-199/Domain: cyclophilin homology <CYP>
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                                                                                                                                                                                                                                                                                                        peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human
N.Alternate names: cyclophilin C
                                    1;
      ed. No. 0.98;
Mismatches
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1; Mismatches
         Pred.
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77.88;
                             7: Conservative
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Best Local Similarity
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Best Local Similarity
Matches 7; Conserv
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79 GYGYKGSKF 87
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                                                                                             1 GFGYKNSKF 9
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A; Molecule type: protein
A; Residues: 1-179 (CH2>
C; Comment: This enzyme catalyzes interconversion of the cis and trans imino peptide b
C; Comment: This enzyme catalyzes interconversion of the cis and trans imino peptide b
C; Cyperfamily: peptidylprolyl isomerase; cyclophilin homology
C; Keywords: cis-trans-isomerase; cyclosportn A binding; cytosol; nucleotide binding;
F; 1-179/Domain: cyclophilin homology (CYP>
F; 81-88/Region: nucleotide-binding motif A (P-loop)
F; 31.712/Ending site: phosphate (Thr) (covalent) (by protein kinase II) #status predicted
F; 23/Ending site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F; 23/Ending site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F; 131/Ending site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F; 132/Binding site: substrate (Thr) #status predicted
F; 132/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
F; 132/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
F; 172/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
F; 172/Binding site: phosphate (Thr) (covalent) (by casein kinase)
F; 172/Binding site: phosphate (Thr) (covalent) (by casein kinase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Fusarium sporotrichioides
C; Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 19-Jan-2001
C; Accession: JT0686; PN0166; JT0702
R; Chow, L. P.: Heno, Y.; Tsugita, A.
submitted to JIPID, June 1995
A; Description: Amino acid sequence of peptidyl-prolyl isomerase a from Fusarium sporo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytosolic - fungus (Fusarium sporotrichioide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotr
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                            A; Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
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                                                                C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Keywords: cis-trans-isomerase; cyclosporin A binding; T-cell F;3-164/Domain: cyclophilin homology <CYP>
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                                                                                                                                                                                                                                    Score 40;
Pred. No.
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A;Residues: 1-41 <FUNA
R;Chow, L.P.; Kamo, M.; Ueno, Y.
submitted to JIPID, August 1995
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Best Local Similarity 77.07
Lea 7; Conservative
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Best Local Similarity 77.87
T. Conservative
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A;Residues: 1-179 <CHO>
R;Fukaya, N.; Chow, L.P.; Su
submitted to JIPID, May 1994
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A; Accession: PN0166
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A; Accession: JT0702
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56 GFGYKGSSF
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C; Function:
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A, Molecule type: mRNA
A, Rolecule type: mRNA
A, Reductions 100-148, "MARPARRSPSPTVGNSNFFDLRAFYPSNH', 'SFCSSGEHPHPICSQYPVISALTEVLWVP', 'YFF
A, Rolecule type: mBL. MARPARRSPSPTVGNSNFFDLRAFYPSNH', 'SFCSSGEHPHPICSQYPVISALTEVLWVP', 'YFF
A, Note: this sequence was corrected by A58859
R, Meyuhas, O.
submitted to GenBank, December 1991
A, Reference number: A58859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptidylprolyl isomerase (EC 5.2.1.8) A - rat
Nichternate names: 13.3 protein [mistacentification]; cyclophilin A; cyclosporin A-bindi
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Sate: 31.Mar.1992 #sequence_revision 31-Mar.1992 #text_change 04-Feb-2000
C; Accession: A59819; A60036; A15622; A58859
R; Danielson, P.E.; Forss-Petter, S.; Brow, M.A.; Calavetta, L.; Douglass, J.; Milner, R.
A; Title: p1B15: A cDNA clone of the rat mRNA encoding cyclophilin.
A; Reference number: A29819; MuID: 88283345
A; Accession: A29819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds C; Superfamily: peptidylprolyl isomerase; cyclophilin homology C; Keywords: cis-trans-isomerase; cyclosporin A binding; DNA binding; macrophage; T-cell; F; 3-164/Domain: cyclophilin homology CYC
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A;Status: nucleic acid sequence not shown; not compared with conceptual translation
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R;Lad, R.P.; Smith, M.A.; Hilt, D.C.
Brain Res. Mol. Brain Res. 9, 239-24, 1991
A;Title: Molecular cloning and regional distribution of rat brain cyclophilin.
A;Reference number: A60036; MUID:91232390
                                                                                                                                                                    DNA binding protein in macrophages.
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                                                  A; Cross-references: GBS NID: 950620; PIDN: CAA36989.1; PID: 950621 R; Krummrel, U; Bang, R.; Schnidtchen, R.; Brune, K.; Bang, H. FEBS Lett. 371, 47-51, 1995 A; Tille: Cyclophilin-A is a zinc-dependent DNA binding protein in macro A; Reference number: S66416; WID: 95394146
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Pred. No. 2.4;
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                                                                                                                                                                                                                                                                 A:Wolecule type: protein
A:Residues: 2-21 KRUD
A:Experimental source: nuclear cyclophilin of H4-7 cells
C;Genetics:
A:Genetics:
C;Function:
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A; Residues: 1-164 <LAD>
A; Experimental source: brain
B; Theodor, L; Peleg, D; Meyuhas, O.
B; Pichin Biophys. Acta 826, 137-146, 1985
A; Title: P31, a mammalian housekeeping protein
A; Reference number: A15632; MUID: 86026347
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Best Local Similarity 77.8%;
Matches 7; Conservative
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A; Residues: 1-164 <DAN>
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A; Residues: 1-164 <MEY>
                                   A, Residues: 1-164 <HAS>
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          A; Molecule type:
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: B30809; S07585
R;Tropschug, M.; Nicholson, D.W.; Hartl, F.U.; Koehler, H.; Pfanner, N.; Wachter, E.; Ne
J. Biol. Chem. 263, 1443-14440, 1988
A;Triber Cyclosporin A-binding protein (cyclophilin) of Neurospora crassa. One gene code
A;Reference number: A92671; MUID:89008293
A;Reference number: A92671; MUID:89008293
A;Residues: 1-223 <TRO>
A;Residues: 1-233 <TRO>
A;Cross-references: GB:303963; NID:9168805; PIDN:AAA33584.1; PID:9168806
A;Rocession: A30809
A;Residues: 44-223 <TRO>
A;Cross-references: GB:303963
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41 GFGYKGSTF 49

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C.Accession: A41581
R.Bergsma, D.J.: Eder, C.; Gross, M.; Kersten, H.; Sylvester, D.; Appelbaum, E.; Cusi
                                                                                                                                                               t, W.P.; Bossard, M.J.; Brandt, M.; Levy, M.A.
J. Balol. Chem., 266, 23204, 23214, 1991
Asfittle: The cyclophilin multigene family of peptidyl-prolyl isomerases. Characteriza A; Reference number: A41581; MUID:92078499.
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                                                   C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 02-Sep-2000
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peptidylprolyl isomerase (EC 5.2.1.8) 3 precursor - human
N;Contains: cyclophilin
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Pred. No. 4.5;
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us-09-720-469-3.rsp

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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2000
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OM protein - protein search, using sw model

January 15, 2002, 13:14:58 ; Search time 24.88 Seconds (without alignments) 13.263 Million cell updates/sec Run on:

Title:

US-09-720-469-3 51 1 GFGYKNSKF 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

100059

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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NEIMB - NEIMB - NEIMB - YEAST - YEAST - XENLA - BOVIN - YEAST - HUMAN - KLEPN - KLEPN	ALIGNMENT: 208 RT; 208 ence upda: RATION UP RA	OP 26-40.  Hunter C relophilin squence."; 1903-1907( Mariller C K., Kocher te protein 191).  ', Sutcliff c cyclophi.	The M., Gee eccorded in epidermal epidermal is calcium seconds.
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                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
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01-WAR-1992 (Rel. 21, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PEPTIDYL-PROINL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
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*X-ray structure of a cyclophilin B/cyclosporin complex: comparison with cyclophilin A and delineation of its calcineurin-binding
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Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                              PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PREVENT SECRETION FROM ER. A814481B7EBD4579 CRC64;
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Pfan, PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSA_PPISKASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PR0SITE; PS0072; CSA_PPIASE_2; 1.
CYGLOSPOTIN; ISOMERASE: Rotamase; Signal; Endoplasmic reticulum; Multigene family; 3D_structure.
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1-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROINE CISS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sclurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B. PREVENT SECRETION FROM ER
                           T,
                 MEDLINE-90300692; PubMed-2194066;
Iwai N., Inagami T.;
"Molecular cloning of a complementary DNA to rat cyclophilin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 51; DB 1; Length 208; 100.0%; Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
Schroeter H., Multhaup G., Nordheim A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NY SIMILARITY).
4BBDF5AE40BAD3A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfan, PF00160, pro_isomerase; 1.
PRNTRS: PR00153; CSAPPISMRASE.
PROSITE: PS00170; CSA_PPIASE_1; 1.
PROSITE: PS0072; CSA_PPIASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92112948; PubMed-1530944;
Arber S., Krause K.-H., Caroni P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kidney Int. 37:1460-1465(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1992 (Rel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 AA; 22713 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M60456; AAA37498.1; -. EMBL; X58990; CAA41736.1; -. PTR; B39722; B39722. P1R; S21835; S21835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS TO C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
208
208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:97750; Ppib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P23284; 1CYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
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26
199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GFGYKNSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein mRNA.
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Conservative
                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                               208 AA;
                                                                                                                                                                                                                              Sest Local Similarity
                                                                                                                                                                                                                                                               77 GFGYKDSKF 85
                                                                                                                                                                                                                                                     1 GFGYKNSKF 9
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_Tax1D=6210;
                                                                                                 P23284;
                                                                                                                                                                                                                                                                                                                                                                                                 Echinococcus
                                                                                                                                                                                                                                     .;
8
                                                                                                                                                                                                                                                                                                            CYPH_ECHGR
P14088;
                                                                                                                                                                                                                       Ouery Match
                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                               SIGNAL
                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                    CYPH_ECHGR
                                                                                                                                                                                                                                     datches
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                     "S-cyclophilin is retained intracellularly via a unique COOH-terminal sequence and colocalizes with the calcium storage protein
                                                                                                                                                                                                                                                                                                      01-00N-1994 (Rel. 29, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PEPTIDYL-PROINE GIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.

By SIGNAL

1 25

By SIMILARITY.
                                                                                                                                                                                                                     0;
                                                                                                                                                                                                   100.0%; Score 51; DB 1; Length 208; 100.0%; Pred. No. 0.02;
                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Carrello A., Mark P.J., House A.K., Ratajczak T.;
Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
                                                                                                                                                           PREVENT SECRETION FROM ER (BY SIMILARITY).
76D12AC3427FEF32 CRC64;
                                                                                                                                                                                                           Pred. No. 0.02;
                                                                                                                                                                                                                                                                                          208 AA.
                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                           PRT;
                                                                                           pfam; PF00160; pro_isomerase; 1.
PROSITE: PS00170; CSA_PPIASE_1: 1.
PROSITE: PS00170; CSA_PPIASE_1: 1.
PROSITE: PS000770; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94283623; PubMed-8013656;
                                                                                      InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                           208 AA; 23025 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS Lett. 347:31-36(1994)
                                                                                                                                                                                                  Ouery Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                            25
208
208
                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cyclophilin-A.";
                                                                            HSSP; P23284; 1CYN
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 26-71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 26-45.
                                                                                                                                                                                                                                            1 GFGYKNSKF 9
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
                 calreticulin.";
                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE ** Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
                                                                                                                                                                                                                                                                                       CYPB_BOVIN
P80311:
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                 CYPB_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ol-NOV-1990 (Rel. 13, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROUV. CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) (FRAGMENT).
Eukarvora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-90014983; PubMed-2677720; Lightowlers M.W., Haralambous A., Rickard M.D.; Amino acid sequence homology between cyclophilin and a cDNA-cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B. PREVENT SECRETION FROM ER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Platyhelminthes, Turbellarian Platyhelminths,
Rhabditophora, Eulecithophora, Revertospermata, Mediofusata,
Neodermata, Cestoda, Eucestoda, Cyclophyllidua, Taeniidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN, SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 1; Length 208; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> G (IN REF. 3).
0097C88289AF6276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                               Interpro: IPR002130; CSA_PPIBASE.
Pfam: PF00160; pro_isomerase; 1.
PRINTS: PR00153; CSAPPISNRASE.
PROSITE: PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25
208 PE
208 PR
30 K
22701 MW;
                                                                                                                                                                                                                                                                                                                               EMBL; D14073; BAA03158.1; -.
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Gaps

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Indels

Mismatches Pred. No.

Conservative

6

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Best Local Similarity
Matches 7; Conserv
                                                                        1 GFGYKNSKF
                                                                                                                                                                                                               CYPC_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYPB_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-00T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
PEPTIDYL-PROVE CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS BEFECTS VIA AN INHIBITORY ACTION ON PPIASE.
-1- SUBCELLULAR LOCATION: CYPOPLASMIC.
-1- TISSUE SPECIFICITY: UBIQUITOUS.
-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blattella germanica (German cockroach).
Eukaryota: Metazoa: Arthropoda: Tracheatu: Hexapoda: Insecta:
Prerygota: Neoptera: Orthopteroidea: Dictyoptera: Blattaria:
Blaberoidea: Blattellidae: Blattellinae; Blattella.
NGBI_TaxID=6973;
                                                                                                                                                                                                                                                                                                         88.2%; Score 45; DB 1; Length 161;
88.9%; Pred. No. 0.19;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclosporin; Isomerase; Rotamase.
SEQUENCE 164 AA; 17935 MW; ASE25B574DFCDC99 CRC64;
                                                                                                                                                                                                                                        161 AA; 17223 MW; 72661E2F4FEF466F CRC64;
                                                                                                                                                                                      Cyclosporin; Isomerase; Rotamase; Multigene family.

NON.TER 1 1 1

SEQUENCE 161 AA; 17223 MW; 72661E2P4FEF466F CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                      HSSP: P05092; 3CYS.
InterPro: IPR002130; CSA_PPIase.
Pfam: PF00160; pro_isomerase; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-96096751; Pubmed-8529654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR002130; CSA_PPIase.
Piam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X87418; CAA60869.1; -. HSSP; P05092; IAWV.
                      EMBL; J04664; AAA29058.1;
PIR; A45000; A45000.
                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 80.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 11111 111
42 GFGYKGSKF 50
                                                                                                                                                                                                                                                                                                                                                                                                      1 GFGYKNSKF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYPH_BLAGE
P54985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
CYPH_BLAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
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DB 1; Length 164;

82.4%; Score 42;

Query Match

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                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL (IS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.
-1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITINE-94304830; PubMed-8031755;
Schneider H., Charara N., Schmitz R., Wehrli S., Mikol V.,
Zurini M.G., Quesniaux V.F., Movva N.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 1; Length 212; 
Pred. No. 0.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclosporin; Isomerase; Rotamase; Multigene family.
SEQUENCE 212 AA; 22763 MW; 6F3DB547A2AE581B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                     212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro: IPR00130; CSA_PPISSE.
Pfam: PF00160; pro_isomerase: 1.
PRNTNS: PR00150; CSAPPISNRASE.
PROSITE: PS00170; CSA_PPIASE_1: 1.
PROSITE: PS50072; CSA_PPIASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S71018; AAB31350.1; -. HSSP; P05092; 2RMC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 82.4%;
Similarity 77.8%;
7; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
||||| |:|
45 GFGYKGSRF 53
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                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GFGYKNSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 GYGYKGSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 123842; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1992 (
01-MAR-1992 (
15-JUL-1999 (
                                                                                                                                                                                                                                                                                                         PPIC OR CYPC.
                                                                                                                                     CYPC_HUMAN
P45877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYPB_CHICK
P24367;
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Bergsma D.J., Sylvester D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INIT_MET
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                          the secretory pathway.";
J. BALOL. CHEM., 266.10739-10742(1991).
GATALYTON. PPIAGES ACCELERATE THE FOLDING OF PROTEINS.
CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS. IN OLGOPEPTIDES.
C. ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
C. SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LOMEN (BY SIMILARITY).
C. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN).
PEPTIDYL-PROLYL CIS-TRANS ISOMBRASE B PRECURSOR (EC 5.2.1.8) (PPIASE) (TOTOMARSE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordara; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                    MEDIINE-91250364; PubMed-2040593; Caroni P., Rothenfluh A., McGlynn E., Schneider C.; "S-cyclophilin. New member of the cyclophilin family associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PREVENT SECRETION FROM ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D9C0C2E528E25B59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P23284; ICYN.
InterPro: IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase: 1.
PRNITS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-90174932; PubMed-2408007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 80.4
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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207
207
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                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 GFGFKGSKF 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10030;
                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GFGYKNSKF 9
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P14851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cricetulus
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        DDB NA REPRESENTED BY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PEPTIDYL-PROINI (SESTRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN) (SP18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                             CSA MEDIATES SOME
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
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MEDLINE-90326555; PubMed-2197604;
Hasel K.W., Sutcliffe J.G.;
"Nucleotide sequence of a cDNA coding for mouse cyclophilin.";
Nucleic Acids Res. 18:4019-4019(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.4%; Score 40; DB 1; Length 163; 77.8%; Pred. No. 1.6; 2; Indels live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 AA; 17768 MW; 02D44F71B8F87A1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclosporin; Isomerase; Rotamase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-19; 21-27 AND 76-84.
                                                                                                                                                                                                                                                                                                                                             HSSP, P05092; 3CYS.
InterPro; IPR002130; CSA_PPIase.
Pfam: PP00160; Pro_isomerase; 1.
PRINTS; PR00133; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                            EMBL; X17105; CAA34961.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                PIR; S07597; CSHYAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Macrophage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 GFGYKGSSF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GFGYKNSKF 9
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by a multigene family

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STRAIN-74-OR23-1A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GFGYKNSKF 9
                                                                                                                            SEQUENCE OF 1-28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAMESHIFTS.
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P10255;
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SEQUENCE
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DT 01-MAR-

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P10.111, P18303;
P10.111, P18303;
P10.14MR-1989 (Rel. 10, Last sequence update)
P10.4MR-1989 (Rel. 32, Last annotation update)
P10.4VV-1995 (Rel. 32, Last annotation update)
CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN) (P31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE. SUBCELLULAR LOCATION: CYTOPLASMICS SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Dankelson P.E., Forss-Petter S., Brow M.A., Calavetta L.,
Danylass J., Milner R.J., Sutcliffe J.G.;
"PIBLS: a cDNa clone of the rat mRNA encoding cyclophilin.";
DNA 7:261-267(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.4%; Score 40; DB 1; Length 163; 77.8%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lad R.P., Smith M.A., Hilt D.C.; "Molecular cloning and regional distribution of rat brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRV -> TXP (IN REF, 2).
AC724D44DBBF4840 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclosporin; Isomerase; Rotamase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brain Res. Mol. Brain Res. 9:239-244(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR002130; CSA_PPIase.
Pfam: PF00160; pro_ISOMETASe; 1.
PRNUTS; PR00153; CSAPPIAMASE.
PROSITE: PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
MEDLINE-91232390; PubMed-1851525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-86026347; PubMed-2996604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theodor L., Peleg D., Meyuhas O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 AA; 17840 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, S10327; CSMSA.
HSSP; P05092; 3CYS.
SWISS-2DPAGE; P17742; MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X52803; CAA36989.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:97749; Ppla.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 GFGYKGSSF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GFGYKNSKF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cyclophilin.
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CONFLICT
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                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-1989 (Rel. 10, Created)
01-WAR-1989 (Rel. 10, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
PEPTIDYL-PROYL CIS-TRANS ISOMERASE PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) (CPH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89008293; PubMed-2971658;
Tropschug M., Nicholson D.W., Hartl F.-U., Kohler H., Pfanner N.,
Wachter E., Neupert W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
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Sordariales; Sordariaceae; Neurospora.
NCBL_TaxID-5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 1; Length 163; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 AA; 17743 MW; DD16D1C980474414 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyclosporin; Isomerase; Rotamase; Multigene family.
"P31, a mammalian housekeeping protein encoded containing a high proportion of pseudogenes."; Blochim. Biophys. Acta 826:137-146(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interproj 1972, 3013.
Interproj IPR002130; CSA_PPIBASe,
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00137; CSAPPIBARASE.
PROSITE; PS00170; CSA_PPIBASE_1; 1
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                           MEDLINE-92287042; PubMed-1599421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M19533; AAA41009.1; -. EMBL; M25637; AAB59719.1; -.
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Best Local Similarity 77،۰۰۰
ایم 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A15632; CSRT31.
PIR; A29819; CSRTA.
HSSP; P05092; 3CYS.
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STRAIN-WISTAR; TISSUB-Skeletal muscle;
Price N.T., Woodfield K.Y., Halestrap A.P.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                         TISSUE-Liver;
MEDLINE-92287042; PubMed-1599421;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 P
206 F
39 M
31 S
30 C
21810 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U68544; AAB08453.1; -. PIR; S23122; S23122.
HSSP; P05092; 3CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 7; Conserv
                                                                          SEQUENCE OF 30-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 GFGYKGSTF 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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                                                                                                                                                                                         PEPTIDE BONDS IN OLICOPEPTIDES.
-!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL AND CYTOPLASHIC.
-!- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS
BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
"Cyclosporin A-binding protein (cyclophilin) of Neurospora crassa. One gene codes for both the cytosolic and mitochondrial forms."; J. Biol. Chem. 263:14433-14440(1988).
                                                                                                                               prolyl cis-trans isomerase of Neurospora crassa.;
Nucleic Acids Res. 18:190-190(1990).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                             "Nucleotide sequence of the gene coding for cyclophilin/peptidyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyclosporin; Isomerase; Rotamase; Mitochondrion; Transit peptide; Alternative initiation.
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR (EC.5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPIASE, MITOCHONDRIAL ISOFORM. PPIASE, CYTOSOLIC ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.4%; Score 40; DB 1; Length 223; 77.8%; Pred. No. 2.1;
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D494AB77F9768AE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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PIR; B30809; CSNCN.
HSSP; P065092; 3CXC.
InterPro; IPR002130; CSA_PPIASE.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                MEDLINE-90174923; PubMed-2137907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 AA; 24064 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J03963; AAA33584.1; -.
EMBL; X17692; CAA35681.1; -.
EMBL; X17692; CAA35682.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 77.5.
77.5.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 GFGYKGSSF 108
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                                                                                                  Fropschug M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYPM_RAT P29117;
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SEQUENCE
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EMBL; EMBL;

RRIEN RRIEN

CHAIN

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Interpro; IPR002130; CSA_PPIase.
PREM: PR00150; PRC_isomerase; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS00072; CSA_PPIASE_2; 1.
PROSITE; PS00072; CSA_
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MEDLINE-92070B192: PubMed-174118;
MEDLINE-92070B192: PubMed-174118;
MEDGISMA D.J., Eder C., Gross M., Kersten H., Sylvester D.,
Appelbaum E., Cusimano D., Livi G.P., McLauglin M.M., Kasyan K.,
Porter T.G., Silverman C., Dunnington D., Hand A., Prichett W.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDYL-PROLYL CIS-TRANS ISOMERASE. MISSING (IN A MINOR FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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01-APR-1993 (Rel. 25, Last sequence update)
120-MG-2001 (Rel. 40, Last annotation update)
120-MG-2001 (Rel. 40, Last annotation update)
120-MG-2011 (Rel. 40, Last Encourage)
120-MG-2011 (Rel.
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                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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P49792; 015280;
01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
(NUCLEOPORIN UP938) (358 KDA NUCLEOPORIN) (P270).
RANBP2 OR NUP9589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-55294031; PubMed-7775481; MEDIINE-55294031; PubMed-7775481; Mu J., Matunis M.J., Kraemer D., Blobel G., Coutavas E.; Mu J., Matunis M.J., Kraemer D., Blobel G., Coutavas E.; "Nup358, a cytoplasmically exposed nucleoporin with peptide repeats, anorgh binding stres, zinc fingers, a cyclophilin A homologous domain, and a leucine-rich region."; J. Biol. Chem. 270:14209-14213(1995).
                                                                                                                                                                                                                                                                                         Cyclosporin; Isomerase; Rotamase; Multigene family; Mitochondrion;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95327194; Pubmed-7603572; Yokoyama N., Hayashi N., Seki T., Nishii K., Hayashida T., Kuma K.L., Miyata T., Fukui M., Nishimoto T., Pante N., Aebi U.; Rajart nucleopore protein that binds Ran/TC4."; Nature 376:184-188(1995).
                                                                                                                                                                                                                                                                                                                      22040 MW; D7C76FID4049F16A CRC64;
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                                                                           -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
                                                                                                                                                                                                                                                                                                                                                                   76.5%; Score 39; DB 1; Length 207; 77.8%; Pred. No. 3;
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                                                                                                                                                                                                                                                                                                               MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Pfam: PF00160; pro_isomerase; 1.
PRNINTS; PR00153; CSAPPIBASE.
PROSITE; PS00170; CSA_PPIBASE_1; 1.
PROSITE; PS00072; CSA_PPIBASE_2; 1.
                                                                                                                                                                                         EMBL; M80254; AAA58434.1; --
PIR; A41581; A41581.
HSSP; P05092; 3CYS.
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Best Local Similarity 77.8
Matches 7; Conservative
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-1. SUBGNIT: PORMS A TIGHT COMPLEX IN ASSOCIATION WITH RANBPI AND THE UBIQUITIN. CONJUGATING ENTRY EZ (UBCS) (BY SIMILARITY).

-1. SUBLILLIAR NANY X-X-F-G AND X-F-X-F-G REPEATS.

-1. SIMILARITY: CONTAINS RANBP-TYPE ZINC FINGERS.

-1. SIMILARITY: CONTAINS A RANBP-TYPE ZINC FINGERS.
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RANBP-TYPE 2.
RANBP-TYPE 3.
RANBP-TYPE 5.
RANBP-TYPE 6.
RANBP-TYPE 6.
RANBP-TYPE 6.
RANBP-TYPE 6.
RANBP-TYPE 7.
RA
X-RAY CRYSTALLOGRAPHY (2.96 ANGSTROMS) OF 1171-1304
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InterPro; IPR000697; RanBPl_WASP.
InterPro; IPR000156; Ran_BPl.
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Pfam; PF00611; TPR; 1.
Pfam; PF00641; zf-RanBP; 8.
PRINES; PR00153; CSAPPISMRASE.
SMART; SM00160; RanBD; 4.
SMART; SW00547; ZnF_RBZ; 8.
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InterPro, IPR001876; Znf-RanBP.
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EMBL; D42063; BAA07662.1; -.
PDB; IRRP; 18-MAY-99.
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Matches 7; Conservative
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SUMMARIES

	Description	088541 rattus norv	Ogbvk5 homo sanien	Ogdevi mus museulu	001490 orbinomyces	O98ue5 xenopus lae	O9xzz5 lumbricus r	Ogavh8 mus so. sun	O9r137 mus musculu	Ogerb9 mesocricetu	025093 hirudo medi	O9cw15 mus musculu	O9czk9 mus musculu	O9fw22 orvza sativ	O9u8k2 periplaneta	09n717 leishmania	_		O02614 leishmania		
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Pfam: PF00160; pro_isomerase; 1.
PRINTS: PR00153; CSAPISNASE.
PROSITE; PS5028—PPLASE_2: 1
SEQUENCE 216 AA; 23713 WW; CE9DAD1544AE72FE CRC64;
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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchi P., Lewis S., Matsuo T., Gissi C., King B., Kochiwa H.,

Ruchi P., Lewis S., Matsuo T., Nikaldo I., Pesole G., Quackenbush J.,

Schriml L.M., Stubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boli C., Fletcher C., Fullia M., Gariboldi M.,

Rownstein M.J., Bull C., Fletcher C., Fullia M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Rayordone P., Ring B., Ringwald M., Rodriguz I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Soya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

A Hayashizaki Y.,

Purchional annotation of a full-length mouse cDNA collection.",
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Mammalia; Eutherla; Rodentla; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases EMBL; BC001125; AAH01125.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2D0410A07AA9E420 CRC64;
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Last annotation update)
                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B).
                                                                                              216 AA
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                                                                                              PRT;
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STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002130; CSA_PPIase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 AA; 23742 MW;
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                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-SKIN, AND MELANOMA;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 100.7
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                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GFGYKNSKF 9
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isomerase.
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                                                                                              Q9BVK5
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                                                 RESULT
Q9BVK5
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNN-2000 (TrEMBLrel. 17, Last annotation update)
PEPTIDYL-PROLYL, CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(CYCLOPHILIN B) (ROTAMASE).
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isomerase; Rotamase; \overline{S}1gnal; Cyclosporin; Endoplasmic reticulum. SIGNAL
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Length 216;
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                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSA (POTENTIAL).
PREVENT SECRETION FROM ER SIMILARITY).
7 A5748C94305BBE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Orpinomyces sp. PC-2.
Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
                                                                                                  ö
    100.0%; Score 51; DB 11; 100.0%; Pred. No. 0.086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 AA.
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                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.
MEDLINE=95223986; Pubmed=7708690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q98UES PRELIMINARY; PKT; Q98UES; 01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neocallimasticaceae; Orpinomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
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88.9%;
         Query Match 100.

Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
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PEDGLENGE 2031730; PubMed-1932134;

Davis T.R., Tabatabui L., Bruns K., Hamilton R.T., Nilsen-Hamilton M.;

Basic fibroblast growth factor induces 373 fibroblasts to synthesize and secrete a cyclophilm-like protein and beta 2-microglobulin.";

Biochim. Biophys. Acta 1095:145-152(1991).

InterPro: IPR00130; CSA_PIDASe.

Pfam; PR00160; pro_isomerse; 1.

SEQUENCE 17 AA; 1785 MW; 11276657FEB240D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colgan J.D., Asmal M., Luban J.;
"Haploinsufficient growth defects, increased Th2 cytokine production and cyclosporine resistance in mice lacking CYPA.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ARI71073; ABD50996.1;
HSSP; P05092; 2CPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                   Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10095;
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomí;
                                                                                                       01-MAY-2000 (TrEMBLRel. 13, Created)
1-MAY-2000 (TrEMBLRel. 13, Last sequence update)
01-UNY-2001 (TrEMBLRel. 17, Last annotation update)
SUPERINDUCIBLE PROTEIN 24, SIP24-CYCLOPHILIN HOMOLOG, PEAK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 11; Length 39;
Pred. No. 1.5;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CYCLOPHILIN A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.4%; Score 40; DB 11
llarity 77.8%; Pred. No. 0.65;
Conservative 0; Mismatches
                                                                     17 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:97749; Ppia.
InterPro: PR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 77.8
Matches 7; Conservative
                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
7; Conservé
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GFGYKGSSF 29
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                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                   090VH8
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                             RESULT
Q9QVHB
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-I. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.
                                                                                                                                                                           SEQUENCE FROM N.A.
Manor T., Yoshizato K.;
*Isolation of genes involved in intestinal remodeling during anuran metamorphosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lumbricus rubellus (Humus earthworm).
Sukaryota: Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
Lumbricina; Lumbricidae; Lumbricus.
NCBI_TaxID=35632;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDVL-PROLYL CIS-TRANS ISOMERASE B (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Sturzenbaum S.R., Morgan A.J., Kille P.;
*isolated from earthworms exposed to Cd-supplemented artificial
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                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 13; Length 104;
Pred. No. 1.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                       Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF170328; AAK11503.1;
                                                                                                                                                                                                                                                                                                                                   104 AA; 11350 MW; 8F6AD1CD1C2FB3E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 AA; 17599 MW; B30D22D660966AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUV-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN A (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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PRUNTS; PR00153; CSAPPISMRASE.
PROSITE: PS00170; CSA_PPIASE_; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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HSSP; P05092; 1CWL.
InterPro; IPR002130; CSA_PPlase.
                                                                                                                                                                                                                                                                                                                                                                                               82.4%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                    Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isomerase; Rotamase.
SEQUENCE 164 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
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77 GYGYKGSKF 85
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45 GFGFKGSKF 53
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SEQUENCE
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ISOMETSE: ROLAMASE.
SEGUENCE 143 AA; 15398 MW; 64FFD82018480A6B CRC64;
                                                                                                PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
InterPro; IPR002130; CSA_PPIase. Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GFGYKNSKF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09CMJ5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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Kornecv S., Blackshaw S.E., Kalser K., Davies J.A.;
Kornecv S., Blackshaw S.E., Kalser K., Davies J.A.;
Kornecv S., Blackshaw S.E., Kalser K., Davies J.A.;
ForDA ilpraties from identified neurons.",
Proc. R. Soc. Lond. B. Biol. Sci. 263:57-62(1996).

-!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
FOLDING OF PROTEINS (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.

-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
TRANS ISOMERASE FAMILY.

EMBL: U36797; ABRADISJI.i; -.

USSP; POS092; ZCPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KITIGHT P., Bai Y., Li X., Machida C.A.;
KITIGHT P., Bai Y., Li X., Machida C.A.;
Mesocricetus auratus cyclophilin partial cDNA coding sequence.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PEPTIDYL.-PROIVE CIS-TRANS ISOMERASES ACCELERATE THE
FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYE CIS-
                                                                                                               O9ERB9;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 17, Last sequence update)
01-MIN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN (FRAGMENT).
Mesocricetus auratus (Golden hamster).
BUKATOQUE; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Annellda; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
NCBI_TaxID=6421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.4%; Score 40; DB 11; Length 70; 77.8%; Pred. No. 2.8; 2; Indels iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 AA; 7841 MW; 472374C1287ACEC9 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN-A (EC 5.2.1.8).
                                                                                                           70 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                       PRT;
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PROUTS: CSAPPISMRASE:
PROSTITE: PS00170; CSA_PPIASE_1; 1.
PROSTITE: PS00170; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANS ISOMERASE FAMILY.
EMBL, AY004869; AAG00259.1; -.
InterPro; IPR002130; CSA_PPIase.
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                       PRELIMINARY;
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24 GFGYKGSSF 32
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10036;
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SEQUENCE
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STRAIN=CSTBL/6J: TISSUE=EMBRYONIC STEM CELLS;

K STRAIN=CSTBL/6J: TISSUE=EMBRYONIC STEM CELLS;

K RWANI J., Shingawa A., Shibbta K., Yoshino M., Itoh M., Ishil Y.,

A RAWANA T., Shingawa A., Shibbta K., Yoshino M., Itoh M., Ishil Y.,

A RIARWA T., Shingawa A., Shibbta K., Yoshino M., Itoh M., Ishil Y.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Radota K., Matsuda H.A., Ashinrar H., Batalov S., Casawar T.,

A Radota K., Matsuda H.A., Ashinrar M., Batalov S., Casawar T.,

A Radota K., Matsuda H.A., Ashinrar M., Batalov S., Casawar T.,

A Radota K., Matsuda H.A., Ashinrar M., Batalov S., Casawar T.,

A Schriml L.M., Staubil F., Staubil F., Baraki B., Kochiwa H.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

A Ustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

A Sashi H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,

A Sashi H., Toyo-Oka K., Wang K.H., Weitz C., Willming L.,

A Wynshaw-Borls A., Yoshida K., Hassgawa Y., Kawaji H., Kohtsuki S.,

A Hassaliaki Y.,

A Hassgawa Y., Kawaji H., Kohtsuki S.,

A Hassgawa Y., Kawaji H., Kohtsuki S.,

A Hassgawa Y., Kawaji H., Kohtsuki S.,
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                                                                            Gaps
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--- SIMILEMETRY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.
TRANS ISOMERASE FAMILY.
EMBL, AKO10649; BAR27089.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001).
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                                                                        ö
    Length 143;
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17984 MW; DIC8D3E825F0392F CRC64;
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Last annotation update)
78,4%; Score 40; DB 5;
77.8%; Pred. No. 5.8;
                                                                                                                                                                                                                                                                                                                                                                                                                    164 AA.
                                                                            0; Mismatches
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
PEPTIDYLPROLYL ISOMERASE A.
                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:97749; Ppia.
InterPro; IPR002130; CSA_PPIase.
                                        Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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DB 11; Length 164;

78.4%; Score 40;

Q9CZK9

RESULT 09CZK9

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Submitted (JAN-1998) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: PEPTIDYL-PROLYCL GIS-TRANS ISOMERASES ACCELERATE THE FOLDING OP PROPEINS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPERTIDES.
-!- SIMILARITY: PELONGY TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.
                                                                               01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO ARABIDOPSIS THALLANA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Hsing Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M.,
Chen C.-S., Shaw J.-F.;
"Oryza sativa PAC P0036D10 genomics sequence, complete sequence.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC073405; AAG03106.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Renucci M., Tirard A., Matarazzo V., Belaich A., Clement J.L.;
"Isolation of a cDNA sequence encoding a peptidyl-prolyl cis-trans
isomerase from Periplaneta americana antennae.";
                                                                                                                                                                    Oryza sativa (Rice).
Ebkaryock: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (FRAGMENT).
Periplaneta americana (American cockroach).
Putaryota; Metazoa; Arthropoda; Tracheata; Hexapoda: Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; NCBI_TaxID=6978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.4%; Score 40; DB 10; Length 173; 77.8%; Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 173 AA; 19158 MW; 28EADE80F4625EB9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002130; CSA_PPIase.
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HSSP; P05092; 2CPL.
InterPro; IPR002130; CSA_PPIASE.
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PRINTS; PR00153; CSAPPISMRASE,
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            PRELIMINARY;
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                                                                                                                                           (P34791) (FRAGMENT).
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                                                                                                                                                                                                                                                              NCBI_TaxID=4530;
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A Arakawa T., Hara A., Fhunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fhunishi Y., Konno H., Adachi J., Fukuda S.,
A Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
Pleischmann W., Gaasterland T., Gissi C., King B., Kochlwa H.,
Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
A Schriml L.M., Staubli F., Szuki R., Tomita M., Wagner L., Washio T.,
A Blake J., Bolinga N., Carninci P., de Bonaldo M.F.,
A Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
Havsaki Z., Yoshida K., Hassegawa Y., Kawaji H., Kohtsuki S.,
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-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinoe; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;
Functional annotation of a full-length mouse cDNA collection.";
Nature 409:665-690(2001).
-!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOLDING OF PROTEINS (BY SIMILARITY).
CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
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                                Indels
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Last annotation update)
                           5;
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       Pred. No. 6.7;
                             Mismatches
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PROSITE; PS50072; CSA_PPIASE_2; 1.
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EMBL, AK01249!; BAB28276.1; -
MGD; MGI:97149; Ppia.
InterPro: IPR002130; CSA_PPIase.
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77.8%;
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                        7; Conservative
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Matches 7; Conservative
                                                                                                                                                                                                                                  PRELIMINARY;
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  Best Local Similarity
Matches 7: Conserv
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                                                                                                 48 GFGYKGSSF 56
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78 AA; 8341 MW; DB73CC5CF97334B0 CRC64;

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STRAIN=FRIEDLIN;

CSTRAIN=FRIEDLIN;

MUTPHY L., Quall M., Harris D., Rajandream M., Ivens A., Barrell B.,

MUTPHY L., Quall M., Harris D., Rajandream M., Ivens A., Barrell B.,

A Oliver K.;

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

-I-FOUGTION: PEPTIDEN CIS-TRANS ISOMERASES ACCELERATE THE

FOLDING OF PROTEINS (BY SIMILARITY).

-I-CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMDIC

PEPTIDE BONDS IN OLIGOREPTIDES.

-I-SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-

TRANS ISOMERASE FAMILY.

REMBL, ALSOULIS CRAPES FAMILY.

REMBL, ALSOULIS
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           01-6CT-2000 (TrEMBLrel. 15, Created)
01-6CT-2000 (TrEMBLrel. 15, Last sequence update)
01-5CT-2000 (TrEMBLrel. 17, Last sequence update)
01-5UN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE CYCLOPHILIN (FRAGMENT).
LM12.959.
Lusishmania major.
Euelshmania major.
Euelshmania major.
Lustryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
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Ouery Match 76.5%; Score 39; DB 5; Length 78; Best Local Similarity 77.8%; Pred. No. 4.7; Matches 7; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                          2 GFGYKGSTF 10
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09N717;
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Gaps 0

Search completed: January 15, 2002, 13:16:25 Job time: 656 sec

30 GFGYANSPF 38

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January 15, 2002, 13:05:27 ; Search time 81.32 Seconds (without alignments) 10.020 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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522463 seqs, 74073290 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 1 GYKNSKFHRVI 11 US-09-720-469-4 60 Perfect score: Scoring table: Sequence: Searched: Title:

Total number of hits satisfying chosen parameters:

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/SIDS8/gcgdata/geneseqg/geneseqp/AA1987.DAT:\* A\_Geneseq\_1101:\* 110:: 111: 112:: 114:: 114:: 116:: 1 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			Description	Human Cost and Human	Homen of croping and	Human Secretary pro	Human cyclophilin	Hillian Cancer accor	Caenorhabditic ole	D discoldenm cvol	Human prostate can	Himan Cyclophilin	Arahidonsis thalis	Arabidopsis thalia
COLUMNICO			ID	AAY69924	AAGOOOGO	AAB73302	AAB73301	AAB43878	AAB49141	AAW80784	AAB56701	AAU01197	AAG16463	AAG05073
				21	21	22	22	21	22	19	21	22	21	21
			Match Length DB	11	166	211	216	291	171	180	183	207	252	254
	œ	Query	Match	100.0	100.0	100.0	100.0	100.0	80.0	80.0	80.0	0.08	80.0	80.0
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AAG16462	AAG05072	AAG16461	AAW54235	AAG54741	AAG15070	AAG48166	AAG29380	AAG15069 .	AAG48165	AAG29379	AAB64737	AAR32353	AAG03830	AAM20480	AAM35140	AAB64736	AAR10763	AAR72917	AAR72961	AAR13726	AAP90431	AAW56028	AAG03831	AAU01195	AAB49136	AAB49137	AAB59530	AAB59512	9	AAB98719		502	AAG30404
21	21	21	19	21	21	21	21	21	21	21	22	14	21	22	22	22	13	16	16	13	10	19	21	22	22	22	22	22	19	22	21	21	21
254	259	260	3224	129	191	192	201	205	506	218	114	212	108	108	108	114	4	145	₹	9	164	9	9	165	$^{\circ}$	7	9	72	4	4	163	9	172
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48	48	48	48	47	47	47	47	47	47	47	46	46	45	45	45	45	45	42	45	45	45	45	45	45	45	45	44	44	44	44	44	44	44
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT

Human cyclophilin B peptide fragment #4. AAY69924 standard; peptide; 11 AA. (first entry) 11-APR-2000 AAY69924; AAY69924 

Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy. Homo sapiens. WO9967288-A1

(SUMU ) SUMITOMO PHARM CO LTD. (ITOH/) ITOH K. 98JP-0178449. 25-JUN-1998;

99WO-JP03360.

24-JUN-1999;

29-DEC-1999

WPI; 2000-116932/10. Gomi S; Itoh K,

Tumour antigen peptides derived from cyclophilin B for treatment and diagnosis of tumours  $\,\cdot\,$ 

Claim 4; Page 50; 64pp; Japanese.

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Page

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Gaps

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Indels

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Mismatches

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Conservative

11;

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Matches
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                                                                                                                                                                                                                                                                                                                                expressed sequence tag; secreted protein; cDNA isolation;
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          This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                               ;
                                                                                                       100.0%; Score 60; DB 21; Length 11; 100.0%; Pred. No. 4.1e-05;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; SEQ ID 4171; 71pp + CD-ROM; English.
                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                          Human secreted protein, SEQ ID NO: 4171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duclert A,
                                                                                                                                                                                                                                      AAG00090 standard; Protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                              gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0122487
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-500381/45.
N-PSDB; AAC00096.
                                                                                                                                                      1 GYKNSKFHRVI 11
                                                                                                       Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                    11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                EST;
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                   06-OCT-2000
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                                                                                                                                                                                                                                                                                                                                Human; 5'
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                                                                                                                                                                                                                                                           AAG00090;
                                                                                                                                                                                                                          AAG00090
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 X8888XX
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Score 60; DB 21; Length 166; Pred, No. 0.00078;

100.0%; 100.0%;

Ouery Match Best Local Similarity

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The invention relates to a composition for modulating somatclactogenic function, comprising cyclophilin B (CypB), a mutant of cyclophilin B (cypB), a mutant of cyclophilin B (cypB), a mutant of cyclophilin B with a cypB mutant in which residues 2-12 of the mature protein are absent) or an inhibitor of the interaction of cyclophilin B with a somatclactogenic hormone (e.g., prolactin, growth hormone). The invention also relates to a method of identifying inhibitors of somatclactogenic functions using CypB and a somatclactogenic hormone, and a method for diagnosing diseases associated with ahormal somatclactogenic functions by assessing diseases associated with ahormal somatclactogenic functions useful for augmenting somatclactogenic function in the animal, and cyclophilin B with a somatclactogenic function in the animal. A composition of cyclophilin B with a somatclactogenic politic of in the treatment of somatclactogenic function in the animal. A composition comprising cyclophilin B with a somatclactogenic of in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprising cyclophilin B cyclophilin B cyclophilin B mutant or a composition comprising cyclophilin B mutant or a composition comprising cyclophilin B mutant or a composition comprising cyclophilin B cyclophilin B mutant or a composition comprising cyclophilin B cyclophilin 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; gigantian; acromegaly; hyperprolactinaemia; C-terminal deletion mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 211;
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Pred. No. 0.001;
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                                                                                                                                                                                                                                                                                                                                                 AAB73302 standard; protein; 211 AA.
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1 GYKNSKFHRVI 11
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                                                     gyknskfhrvi
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AAB43878 standard; Protein; 291 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a composition for modulating somatolactogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactopentc function medulacto; immunosuppression; short stature; muscla wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; gigantism; acromegaly; hyperprolactinaemia.
              Gaps
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       Indels
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       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cyclophilin B (CypB),
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Matches 11; Conservative
                                                                                                  WPI; 2001-211249/21.
                                                              1 GYKNSKFHRVI 11
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Include: cytostatic; proliferative; vulnerary; immunomodulator; antidathetic; coagulat; dermatological; neuroprotective; cardiant; thrombolytic; coagulat; nootropic; antipsoriatic and antidathetic; The proportion of polymucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polymucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune cells, to treat disorders of haematopoietic cells, autoimmune cells, to treat disorders of haematopoietic cells, autoimmune cells, to treat disorders or thrombolytic activity, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78451 and AAB4440 represent sequences used in the exemplification of
                                                                                                                                                                      diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antilhicamatory; antithyroid; antithyroid; antibaterarial; cardiant; dermatological; neuroprotective; thrombolytic; coaqulant; noctropic; vasotropic; antipscriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; heemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer \cdot
                                                                                                                                                         cancer associated gene; cancer antigen; detection; cancer;
                                                                                                   Human cancer associated protein sequence SEQ ID NO:1323.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAR-2000; 2000WO-US05882.
                                                08-FEB-2001 (first entry)
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291 AA;

Sequence

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Gaps

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100.0%; Score 60; DB 22; Length 216; 100.0%; Pred. No. 0.001; live 0; Mismatches 0; Indels (

Ouery Match 100.8 Best Local Similarity 100.8 Matches 11; Conservative

1 GYKNSKFHRVI 11

Rogers MJ;

Ji X,

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Dictyostellum: DP1; discoidin II; human DP1; hDP1; cyclophilin; DdCyP2; bisphosphonate binding protein; calcium metabolism; cyclosporine; osteoporosis; hypercalcaemia; bone metabolism; bone metastases.
                                                                                                                                                                                                                                                                             Bisphosphonate binding protein - used to treat calcium metabolism disorders, including bone metabolism, hypercalcaemia, bone
                                                                                                                                                                                                            Cook JS, Ebetino FH, Ibbotson KJ, Russell RGGR, Watts DJ, Xiong XJ;
D. discoideum cyclophilin (DdCyP2).
                                                                                                                                                                                      (UYSH-) UNIV SHEFFIELD MED SCHOOL.
                                                                                                                                                                                                                                                                                                                         Claim 5; Fig 21; 98pp; English
                                                                                                                                                                                                                                                                                                   metastases, and osteoporosis
                                                                                                                                  98WO-US02709
                                                                                                                                                       97US-0039738
                                                                                                                                                                            (PROC ) PROCTER & GAMBLE CO
                                                                  Dictyostelium discoideum
                                                                                                                                                                                                                                             WPI; 1998-506311/43.
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Matches 8; Conserv
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64 ykdskfhrii 73
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                                                                                                             20-AUG-1998.
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                                                                                                                                                                                                                                                                                                                                                                                           Novel cyclophilin, endogenous to e.g. Dirofilaria immitis, useful for identifying compounds and for treating parasitic infections which are not susceptible to cyclosporin A, comprises a tyrosine residue in drug-binding site
             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a cyclophilin including a tyrosine residue in the drug-binding site, and which is endogenous to the parasites onchocerca volvulus, Brugaia malayl, Dirofilaria immitis. The cyclophilin is useful for inhibiting the growth and development of parasites or for treating parasitic infections which are not susceptible to cyclosporin A. The purified 'tyrosine-containing' cyclophilin can be used to produce antibodies, either polyclonal or monoclonal, useful as probes to detect and/or purify related cyclophilins in other parasites.
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Pred. No. 0.15;
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             Indels
 Pred. No. 0.0014;
Mismatches 0;
                                                                                                                                                                               Caenorhabditis elegans cyclophilin CeCyp-4.
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                                                                                                              AAB49141 standard; Protein; 171 AA
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90.0%;
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               11; Conservative
                                                                                                                                                                                                    Cyclophilin; tyrosine;
                                                                                                                                                                                                                          Caenorhabditis elegans
                                              162 gyknskfhrvi 172
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                                  1 GYKNSKFHRVI 11
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Matches 9; Conserv
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| 55 ykgskfhrvi 64
   Best Local Similarity
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                                                                                                                                                         08-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                            CKS,
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                                                                                                                                    AAB49141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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b
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              Matches
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This represents the amino acid sequence of cyclophilin (DdCyP2) from the Dictyostellum discoldeum Ax-2. The invention provides sequences encoding Dictyostellum DP1, human DP1 (hDP1) and Dictyostellum cyclophilln (DdCyP2) which are bisphosphonate inding proteins The invention also provides methods for purifying and producing such bisphosphonate binding protein. The bisphosphonate binding protein, or an antibody which binds protein can be used in the diagnosts of calcium metabolism disorders. They can also be used to treat calcium metabolism where the treatment is for the regulation of bone metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; prollferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                hypercalcaemia, bone metastases, and osteoporosts, especially by regulation of bone metabolism via interaction with cyclosporine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19; Length 180;
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Pred. No. 0.16;
2; Mismatches
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Conservative
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The present sequence represents human cyclophilin D which is a mitochondrial core component. Cyclophilins interact with other mitochondrial core components e.g. adenine nucleotide translocator (ANT) to proteins to requiate MPT. ANT proteins are mitochondrial permeability translition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination; sequence.
                                                                                                                                                                                                                       New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynuclectide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule
                                                                                         Wiley SE, Andreyev AY, Frigeri LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 22; Length 207;
Pred. No. 0.19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG16463 standard; Protein; 252 AA.
                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 8; 186pp; English.
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81.8%;
  99US-0434354
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                                                                                       Murphy AN, Clevenger W,
Velicelebi G, Davis RE;
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Best Local Similarity
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89 qykqstfhrvi 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 AA;
                                                                                                                                                                                N-PSDB; AAS05937
                                             (MITO-) MITOKOR
03-NOV-1999;
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05-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAPI5566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB55363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antilnfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pollmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAP16506 to AAF16514 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, adenine nucleotide translocator; ANT; MTP; cyclophilin D;
mitochondrial permeability transition pore component; cell survival;
mitochondrial core component; mitochondrial related disorder; cancer;
Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                   Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Pred. No. 0.17;
0; Mismatches
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                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
(ROSE/) ROSEN C A.
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81.8%;
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Matches 9; Conservative
                                                                                                                                                                                                                                                         Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                  WPI; 2000-587513/55
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            WO200055174-A1
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                                                       21-SEP-2000
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28-JUN-1999;
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Pred. No. 0.23;
1; Mismatches
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99US-0157865.
99US-0158029.
99US-015816929.
99US-0158169.
99US-0159293.
99US-0159293.
99US-0159293.
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99US-012548.
99US-0125788.
99US-0126264.
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99US-0161993.
99US-0162142.
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Best Local Similarity 72.7%;
Matches 8; Conservative
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99US-0144814.
99US-0145086.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 0.24;
0; Mismatches
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Pred. No. 0.24;
1; Mismatches
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99US-0134256.
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8; Conservative
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PR 18 - JUL 1999; 99US - 015804

PR 19 - JUL 1990; 99US - 0
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                                                                                                                                                                   Mismatches
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           990S-0161404
990S-0161405
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                                                                                                             Gaps
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                                                                           Score 48; DB 21; Length 260;
Pred. No. 0.24;
1; Mismatches 2; Indels
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99US-0161920.
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Best Local Similarity 72.7%;
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## ALIGNMENTS

MOLECULE TYPE: protein US-08-482-728A-10	ž
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Nuclear , Albritt , Suite 3 28A 0/DJB/RMS	Nuclear , Albritt , Suite 3 28A 0/DJB/RMS
Nuclear , Albritt , Suite 3 28A 0/DJB/RMS	Nuclear , Albritt , Suite 3 28A 0/DJB/RWS
ATTON: ATTON: ATTON: ATTON: Fisher, Joseph Payan, Donada Payan, Donada Payan, Donada Payan, Donada Payan, Donada Bayan, Donada Bayan, Donada Bayan, Donada Bayan, Donada Bayan, Donada Barten Fiehr, Hohbach, Test, Albritte Fiehr, Hohbach, Test, Albritte Francisco Ilfornia Juited States Ilfornia Juited States Francisco Francisco Francisco Bateria Release #1.0, Version CATION DATA: BANDARA: ANUMER: US/08/482,728A BY INFORMATION: ANUMER: 38,304 MINABER: 38,304 MI	ATTON: ATTON: ATTON: ATTON: Fisher, Joseph Payan, Donald Enbr. Hohbach, Test, Albritte Flehr, Hohbach, Test, Albritte Flehr, Hohbach, Test, Albritte Flehr, Hohbach, Test, Albritte Flehr, Francisco Dour Enbarcadero Center, Suite 3 Flencisco Ilfornia Informia In
Nuclear , Albritt , Suite 3 28A 0/DJB/RMS	1482-7284-10 ence 10, Application US/08482728A nt No. 5968802 PPLICANT: Risher, Joseph PPLICANT: Risher, Joseph PPLICANT: Payan, Donald TTLE OF INVENTION: No. 5968802el Nuclear ORRESPONDENCE ADDRESS: 2 ADDRESSEE: Flehr, Hobbach, Test, Albritt ADDRESSEE: Rethr. Hobbach, Test, Albritt ADDRESSEE: Rethr. Hobbach, Test, Albritt ADDRESSEE: Flehr Hobbach, Test, Albritt ADDRESSEE: Albrital ADDRESSEE: Albrital ADDRESSEE: Albrital ADDRESSEE: Albrital ADDRESSEE: ADD

Oucry Match
100.0%; Score 60; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps

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TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 2; Length 126
Pred. No. 0.0072;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                    E: & Herbert
Four Embarcadero Center, Sulte 3400
ADDRESSEE: Flehr, Hobbach, Test, Albritton
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAM: (415) 398-3249
TELEFRAM: 310 277599
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08145995A
Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 130 WATER STREET CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 amino acids
                                                                                                   COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 90.0
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-482-728A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MASSACHUSETTS
                                                               CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                 California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 GYRGSKFHRVI 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: un)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GYKNSKFHRVI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                 APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Payan, Donald
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PATENTEN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE:
CLASSIFICATION: 435
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
RTIOR APPLICATION NUMBER: US 07/740,375
PILING DATE: 05-JAN-1993
APPLICATION NUMBER: US 07/740,375
PILING DATE: 05-JAN-1993
ATTORNEY/AGENT INFORMATION:
RAME: Dunn, Tracy D. REGISTRATION NUMBER: 34,587
REFERENGE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34,587
ER: 5490A-92-1
                                                                                                                        Sequence 7, Application US/08142897
Patent No. 5447852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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100.0%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.

Best Local Similarity 100.

Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-142-897-7
                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 GYKNSKFHRVI 40
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                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94105
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                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                        US-08-142-897-7
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Best Local Similarity 81.8%; Pred. No. 0.014; Matches 9; Conservative 1; Mismatches
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81,8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                        STREET: 130 WATER STREET CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 161 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 81,8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-134-852-13
                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                          1 GYKNSKFHRVI 11
                                                                                  1 GYKNSKFHRVI 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-08-482-728A-12
                                                                                                                                                                    US-09-134-852-13
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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STREET: 32 TOZER ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08451747
Patent No. 5821107
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                          88.3%; Score 53; DB 1; Length 161; 81.8%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
CLASSIFICATION: 514
ATTORIEY AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REFERENCE/DOCKET WUMBER: 30901
REGISTRATION NUMBER: 30901
TELECOMMUNICATION INFORMATION:
TELECHOME: (508) 927-5054
TELEFAX: (508) 927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
REFERENCE/DOCKET NUMBER: 43406
              TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.8 Matches 9; Conservative
                                                                                                                                                            STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-145-995A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-451-747-13
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                                                                                                                                                                                                                                                                                                                                              1 GYKNSKFHRVI 11
                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: unh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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DB 2; Length 161;

88.3%; Score 53;

Query Match

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  Gaps
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Patent No. 6127148
GENERAL INFORMATION:
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: OMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 53; DB 3; Length 161;
Pred. No. 0.014;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0-027-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESINICK, DAVID S.
REGISTRATION NUMBER: 34.346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3440
TELEPHONE: (617) 523-3440
TELERA: (617) 523-3440
TELEX: 200291 STRE UR
TELEX: S00291 STRE UR
TELEX: S00291 STRE UR
TELEX: S00291 STRE UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence I2, Application US/08482728A Patent No. 5968802 GENERAL INFORMATION:

GENERAL Wang, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang, Bruce
Fisher, Joseph
Payan, Donald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC TITLE OF INVENTION: COMPOUNDS NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                      NAME: Dunn, Tracy D. REGISTRATION NUMBER: 34,587
RECERRENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-326-2402
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
LLING DATE: US 08/005,917
PRIOR APPLICATION DATA:
RELIGATION NUMBER:
                                                                                                                           APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-08-145-995A-9
; Sequence 9, Application US/08145995A
; Patent No. 5482850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: RESUICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 434(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-440
TELEFAX: (617) 523-6440
TELEFAX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 164 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 163 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS: unknown unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEOUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-142-897-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GYKNSKFHRVI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 GYKGSSFHRII 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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Sequence 8, Application US/08142897

Sequence 8, Application US/08142897

Sequence 8, Application GENERAL INFORMATION:

APPLICANT: Friedman, Joffrey S.

APPLICANT: Friedman, Irving L.

TITLE OF INVENTION: No. 544852el Cyclophilins, Associating Proteins ITLE OF INVENTION: and Uses

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS: 10

CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                          No. 5968802el Nuclear Cyclophilin
21
                                                                                                                                                                                                                                                                                                                                           COMPUTER READALT TOWN:

WEDIUM TYPE: Floppy disk
COMPUTER: LIBM FC COMPAILINE
OPERATING SYSTEM: PC-TOS/MS-DOS
OSTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION NUMBER: A-61230/DJB/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/142,897
                                                                                                                           ADDRESSEE: Flehr, Hohbach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.08
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 781-1989
TELEFAX: (415) 588-3249
TELEX: 910 277299
INFORMATION FOR SEO ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
COUNTRY: United States
2IP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-482-728A-12
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                    TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 GYKGSTFHRVI 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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2; Indels

Length 163;

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GENERAL INFORMATION:
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                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-09-028-366-7
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                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: GREGORY D. WILLIAMS; NEW ENCLAND BIOLABS, INC. STREET: 32 TOZER ROAD
                                                                                                                                                                                                                                                                                       APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SECURECES: 21
CORRESPONDENCE ADDRESS:
                                                     DB 1; Length 164; 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 164;
                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB 2,
Pred. No. 0.12;
                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
RECISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMONICATION INFORMATION:
TELEPAX: (508) 927-5054
                                                     Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993
CLASSIFICATION: 514
                                                                                                                                                                                                                                      Sequence 9, Application US/08451747
Patent No. 5821107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 9, Application US/09134852
; Patent No. 6127148
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72.7%;
                                                    80.0%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
                                 Query Match
Best Local Similarity 72.77
"... 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 80.0
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-451-747-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
                                                                                                                                         ||| | ||| |||| 47 GYKGSSFHRII 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: unk
                                                                                                                   1 GYKNSKFHRVI 11
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47 GYKGSSFHRII 57
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                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 01915
US-08-145-995A-9
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Gaps
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                              METHOD FOR IDENTIFYING ANTI-PARASITIC COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 164;
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                                                                                                                 ADDRESSEE: DAVID G CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09028366

Patent No. 6150501

GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: HONG, XIQIANG
APPLICANT: MA, DONG
TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Felease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: New England Biolabs, Inc.
STREET: 32 Tozer Road
CITY: Beverly
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAYID S.
REGISTRATION NUMBER: 34235
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S. APPLICANT: PAGE, ANTONY TITLE OF INVENTION: METHOD FOR I TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.08;
                                                                                                                                                      130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-134-852-9
                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                           CITY: BOSTON
                                                                                                                                                                                                                    USA
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Gaps
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                                                                                                                                                   Length 3224;
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                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KEESEE, SUSAN
APPLICANT: KEESEE, SUSAN
APPLICANT: OBAR ROBERT
APPLICANT: WIN YING-JYE
TITLE OF INVENTION: METHOUS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: DETECTION OF CERVICAL CANCER
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thiboault
STREET: 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB 3;
Pred. No. 2.6;
I; Mismatches
                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: GREENHALGH, DUNCAN A
REGISTRATION NUMBER: 38,678
REFERENCE/DOCKET WUMBER: MTP-023 (8395/27)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                      Pred. No. 2.6;
                                                                                                                                                                                      1; Mismatches
                                                                                                                                                     Score 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/989,045 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 15, Application US/08482728A
                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/08989045; Patent No. 6027905; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                 80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 3224 amino acids
                                                                                                                                                   Query Match 80.0 Best Local Similarity 81.8 Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 80.0
Best Local Similarity 81.8
Matches 9; Conservative
                                                     TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-705-660-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3107 GFKNSIFHRVI 3117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYKNSKFHRVI 11
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                  TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                              1 GYKNSKFHRVI 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boston
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US-08-482-728A-15
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                                                                                                                                                                                                                                                                                                                           RESULT 14
US-08-989-045-34
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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: REEEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: DETECTION OF CERVICAL CANCER
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/705,660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: GREENHALGH, DUNCAN A
REGISTRATION NUMBER: 38,678
REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48; DB
Pred. No. 0.12
0; Mismatches
                  OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ VECSION 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,366
                                                                                                                                                                                                                                                    NEB-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34, Application US/08705660 Patent No. 5858683
                                                                                                                                                                                                         NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 978-927-5054
TELEFAX: 978-927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 34:, SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0%;
90.0%;
IBM Compatible
                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 80.0
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-028-366-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 424
COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 YKNSKFHRVI 11
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                                                                                           FILING DATE
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US-08-705-660-34
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STATE: MA
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GENERAL INFORMATION:

APPLICANT: Wang, Bruce
APPLICANT: Wang, Bruce
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr, Hobbach, Test, Albritton
ADDRESSE: Reher the ADDRESSE: Reher the Barcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
21P: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: LIM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRETT APPLICATION DAPA:
APPLICATION NUMBER: US/08/482,728A
FLILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 38,304
RETERENCE/DOCKET NUMBER: A-61230/DJB/RWS
TELECOMMUNICATION INFORMATION:
NAME: Silva, Robin M:
REGISTRATION NUMBER: A-61230/DJB/RWS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 126;
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Search completed: January 15, 2002, 13:03:59 Job time: 215 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

January 15, 2002, 13:06:15; Search time 42.04 Seconds (without alignments) 19.931 Million cell updates/sec

US-09-720-469-4 60 1 GYKNSKFHRVI 11 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database :

1: pirl:\* 2: pirl:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMAPTES

S.	Description	ost [v[craf vdriden								_									۲.	0	peptidylprolyl iso	_	peptidylprolyl iso	peptidylprolyl 1so		peptidylprolyl iso	_	_		ģ.
SUMMARIES	CI CI	S71547	CSHUB	A56861	A54204	A45000	T39632	863995	A40516	T18578	S68767	CSHYAC	CSMSA	CSRTA	JT0686	T21587	A41581	CSNCM	B53422	558884	T50837	T02489	T18573	CSCK	B38388	A40047	CSBOAB	CSPGA	CSHUA	F64808
	DB	7	П	N	C)	7	7	7	7	~1	7	-	П	Н	C.	C\$	7	1	N	7	C)	N	7	-	N	2	7	-	-	7
	Length	183	208	216	212	161	173	164	207	183	137	164	164	164	179	204	207	223	260	3224	201	201	201	162	165	212	163	163	165	199
dР	Query	100.0	100.0	100.0	90.0	88.3	88.3	85.0	83.3	81.7	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	78.3	78.3	78.3	76.7	76.7	76.7	75.0	75.0	75.0	75.0
	Score	09	9	9	54	53	53	51	20	49	48	48	48	8	48	48	48	48	48	48	47	47	47	46	46	46	45	45	4.5	45
	Result No.	П	7	ო	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

peptidylprolyl iso	_	rolvi	7.	peptidylprolyl iso	_	_		7	7	prolyl	_		) LO		>-
538324	862327	T10056	T06073	S51497	S71849	S66681	528020	T27371	T27882	S71219	T27373	T27034	T23003	T21487	CSBY
N	~	~	N	~	~	-	7	7	~	7	7	2	~	7	<b>-</b>
225	356	172	172	180	227	301	165	171	172	173	173	192	523	795	162
75.0	75.0	73.3	73.3	73.3	73.3	73.3	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	0.07
45	45	44	44	44	44	44	43	43	43	43	43	43	43	43	42
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 \$7.1547 nentidylaroly isomerase (FC 5 2 1 8) B 20 2Vt	Potenty pages 1. sometages (L. 3.1.19) b. 20.3N Tau N;Alternate names: cyclophilin B; PPIASE C;Species: Rattus norvegicus (Norway rat)	<pre>C;Date: 15-Nov-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999 C;Accession: S71547</pre>	R:Ruecknagel, K.P.; Pfeifer, T.; Rahfeld, J.U.; Schaerfke, M.; Fischer, G. submitted to the Protein Sequence Database. November 1996	A;Reference number: S71547 A;Accession: S71547	A;Molecule type: protein A;Residues: 1-183 <rue></rue>	A: Experimental source: liver C: Superfamily: peptidylprolyl isomerase; cyclophilin homology	C; Keywords: cis-trans-isomerase
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Fil183/Product: peptidylprolyl isomerase, isoform 20.3K #status experimental <MAT> F;10-172/Domain: cyclophilin homology <CYP>

Gaps ö Query Match 100.0%; Score 60; DB 2; Length 183; Best Local Similarity 100.0%; Pred. No. 0.00044; Matches 11; Conservative 0; Mismatches 0; Indels 0; Mismatches

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1111111111 54 GYKNSKFHRVI 64 1 GYKNSKFHRVI 11 g ò

N RESULT

peptidylprolyl isomerase (EC 5.2.1.8) B precursor (validated) - human Nictornate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin C;Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 08-Dec-2000 C;Accession: A39118 A39722. A40515: S65742 Proc. Natl. Acad. Sci. 0.5.2. A40515: S65742 Proc. Natl. Acad. Sci. 0.5.3. 8, 1903-1907, 1991 A7title: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl iso A;Reference number: A39118; MUID:91156714

A:Molecule type: mRNA A:Residues: 1-208 <PRI> A:Cross-references: GB:Mo0857; NID:g181334; PIDN:AAA52150.1; PID:g181335 R:Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G. Mol. Cell. Biol. 11, 3494-3491, 1991 A:Fitle: An endoplasmic reticulum·specific cyclophilin. A:Reference number: A39722; MUID:91260697

A;Molecule type: mRNA A;Residues: 1-208 <HAS> A;Cross-references: GB:M60457; NID:9181249; PIDN:AAA35733.1; PID:9181250

Gaps

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Indels

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C. Accession: A54204
R:Schneider, H.; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zurini, M.G.; Quesn Blochmistry 33, 8128-8224, 1994
A:Title: Human cyclophilin C: primary structure, tissue distribution, and determinati. A3:Reference number: A54204; MUID:94304830
                                                                                                                                              A)Cross-references: EMBL:X58990; NID:953034; PIDN:CAA41736.1; PID:953035
C:Comment: This protein is distinguished from peptidylprolyl isomerase A by the prese
C:Superfamily: peptidylprolyl isomerase: cyclophilin homology endoplasmic reticulum; T-cell
C;Reywords: cis-trans-isomerase; cyclosporin A binding; endoplasmic reticulum; T-cell
F:1.31/Domain: signal sequence #status predicted <SIG>
F:34-216/Product: peptidylprolyl isomerase B #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Homo sapiens (man)
C:Date: 22-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: sequence extracted from NCBI backbone (NCBIN:149387, NCBIP:149388)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB:S71018; NID:g547303; PIDN:AAB31350.1; PID:g547304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human N;Alternate names: cyclophilin C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 60; DB 2; 100.0%; Pred, No. 0.00053; ive 0; Mismatches 0;
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Pred. No.
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A54204
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-212 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 10; Conserv
                                                                                                                     A; Residues: 9-216 <NOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary A; Molecule type: mRNA
                             A; Status: preliminary A; Molecule type: mRNA
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R; Splk, G.; Haendler, B.; Delmas, O.; Mariller, C.; Chamoux, M.; Maes, P.; Tartar, A.; M. J. Biol. Chem. 266, 10735-10738, 1991
A; Title: A novel secreted cyclophilin-like protein (SCYLP).
A; Receasion. Ad0515; WUID:91250363
A; Accession. Ad0515; WUID:91250363
A; Mccession. Ad0515
A; Mccession. Ad0516
A; Mariller, C.; Allain. F; Kouch, M.; Spik, G.
B; Mariller, C.; Allain. F; Kouch, M.; Spik, G.
B; Mccession. S6734
A; Mccession. S6744
A; Mccession. S6
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NiAlternate names: cyclophilin B; cyclophilin-S1; cyclosporin A-binding protein
C; Species: Wis musculus (house mouse)
C; Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 16-Jul-1999
C; Accession: A56861; B39722; S21835
R; Schumacher, A: Schroter, H: Multhaup, G:; Nordhelm, A.
Biochim. Blophys. Acta 1129, 13-22, 1991
A; Title: Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a putative sign A; Reference number: A56861; MUID:92096454
A; Accession: A56861
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-216 csCH
A; Residues: 1-216 csCH
A; Residues: L-216 csCH
A; Residues: L-216 csCH
A; Residues: L-216 csCH
A; Residues: J-216 csCH
A; Residues: L-216 csCH
A; Residu
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R;Nordheim, A.
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100.0%; Pred. No. 0.00051;
iive 0; Mismatches 0;
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A;Reference number: S21835
A;Accession: S21835
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Best Local Similarity 100.

Matches 11; Conservative
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A; Residues: 9-216 <HAS>
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Peptidylprolyl isomerase (EC 5.2.1.8) [similarity] - tapeworm (Echinococcus granulosu N;Contains: cyclophilin (Schedes: Behinococcus granulosus C;Species: Bchinococcus granulosus C;Species: Bchinococcus granulosus C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 08-Sep-2000 C;Accession: A45000 MW; Haralambous, A.; Rickard, M.D. R;Lightowhers, M.W.; Haralambous, A.; Rickard, M.D. MOL Biochem. Parasitol: 36, 287-289, 1989 MAD. Biochem. Parasitol: 36, 287-289, 1989 MS;Tille: Amino acid sequence homology bctween cyclophilin and a cDNA-cloned antigen o A;Reference number: A45000; MUID:90014983
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A; Cross-references: GB: J04664; NID: 9158843; PIDN: AAA29058.1; PID: 9158844
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A.Map position: 15q21-15q22
C.Superfamily: peptidyprolyl isomerase; cyclophilin homology
C.Keywords: cis-trans-isomerase; cyclosporin A binding
F:37-199/Domain: cyclophilin homology <CYP>
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F.Caroni, P.; Rothenfluh, A.; McGlynn, E.; Schneider, C.
J. Biol. Chem. 266, 10739-10742, 1991
A;Title: S-cyclophilin. New member of the cyclophilin family associated with the secr
A;Reference number: A40516; MUID:91250364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptidylprolyl isomerase (EC 5.2.1.8) cyp-11 [similarity] - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.Contains: cyclophilin
C.Species: Genorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C.Accession: T18578; T24269
R.Page, A.P.; MacNiven, K.
                                                                                                                                                                                                     peptidylprolyl isomerase (EC 5.2.1.8) (S-cyclophilin) precursor - chicken (S-Species: Gallus (chicken) (C.Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999 (S.Accession: A40516
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A; Cross references: GB:M6353; NID:g212648; PIDN:AAA49064.1; PID:g212649
C; Superfamily: peptidylprolyl isomeraes: cyclophillin homology
C; Keywords: cis-trans-isomeraes: cyclosporin A binding
F;34-196/Domain: cyclophilln homology cCYP>
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ilarity 81.8%; Pred. No. 0.041;
Conservative 1; Mismatches
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A;Molecule type: mRNA
A;Roides: 1-183 <PAG>
A;Cross-references: EMBL:U34955; PIDN:AAC47115.1
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Pred. No. 0.056;
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A; Reference number: 218986
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81.8%;
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A; Introns: 34/3; 87/3; 148/1
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Best Local Similarity
'-has 9; Conserva
                                               47 GYKGSRFHRVI 57
                    GYKNSKFHRVI 11
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                            Peptidylprolyl isomerase (EC 5.2.1.8) u-snrnp-associated SPBC1709.04c [similarity] - fis N. Contains: cyclophilin C.Species: Schlzosaccharomyces pombe C.Species: Schlzosaccharomyces pombe C.Species: Schlzosaccharomyces pombe C.Species: O3-Dec-1999 #text_change O8-Sep-2000 C.Accession: T39632 R.Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M. Submitted to the EMBL Data Library, October 1998 A. Reference number: Z21868 A. Reference number: Z21868 A. Reference number: Z21868 A. Scatus: preliminary; translated from GB/EMBL/DDBJ A. Status: preliminary; translated from GB/EMBL/DDBJ A. Status: preliminary; translated from GB/EMBL/DDBJ A. Scatus: preliminary; acid a. M. A. Residues: 1.133 c. Ziv. A. M. A. Residues: 1.133 c. Ziv. A. M. A. Residues: Ind. A. Status: SpDB:SPBC1709.04c A. Map position: 2 A. Gene: SpDB:SPBC1709.04c A. Map position: 2 A. Gene: SpDB:SpBC1709.04c A. Map position: C. Superfamily: peptidylprolyl isomerase; cyclophillin homology C. Keywords: cis-trans-isomerase F. 4-173/Domain: cyclophillin homology cCYPP>
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NiAlternate names: cyclophilin
C; Species: Blattella germanica (German cockroach)
C; Species: Blattella germanica (German cockroach)
C; Date: 20-Jul-1966 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C; Accession: 863995
R; Martinez-Gonzalez, J.; Hegardt, F.G.
Rut: J. Biochem. 234, 284-292, 1995
A; Title: Characterization of a cDNA encoding a cytosolic peptidylprolyl cis-trans-isomer A; Reference number: 863995; MuID:96096751
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-164 «MAR»
A; Residues: 1-164 «MAR»
A; Residues: L-164 «MAR»
A; Residues: cis-trans-isomerase; cyclophilin homology
C; Keywords: cis-trans-isomerase
F; 3-164/Domain: cyclophilin homology <CYP>
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                                                                                                                                             Length 161;
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                                                                                                                                          Score 53; DB 2; Length 161
Pred. No. 0.0084;
1; Mismatches 1; Indels
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Keywords: cis-trans-isomerase F;1-161/Domain: cyclophilin homology <CYP>
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Pred. No. 0.009;
1; Mismatches
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Best Local Similarity 81.8%; Pred. No. (
Matches 9; Conservative 1; Mismatcl
                                                                                                                                          88.3%;
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Best Local Similarity 81.8
Matches 9; Conservative
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54 GYKNSTFHRII 64
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Matches 9; Conserv
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peptidylprolyl isomerase (EC 5.2.1.8) A - rat
N'Alternate names: 13.3K protein [misidentification]; cyclophillin A; cyclosporin A-bi
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A28192 #sequence_revision 31-Mar-1992 #text_change 04-Feb-2000
C;Accession: A29819; A60036; A15632; A58859
DNA 7, 261-267, 1988
A;Title: plabls: A cDNA clone of the rat mRNA encoding cyclophillin.
A;Reference number: A29819; MUID:88283345
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A:Residues: 100-148, MarparrspsptvGnsnFFDLRAFYPSNH','SFCSSGBHPHPICSOYPV1SALTEVLWVP','
A:Cross-references: EMBL:M25637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: catalyzes the cis-trans isomerization of peptidylprolline peptide bonds C; Superfamily: peptidylprolyl isomerase; cyclophilin homology C; Reywords: cis-trans-isomerase; cyclosporin A binding; DNA binding; macrophage; T-ce F; 3-164/Domain: cyclophilin homology <Cyp.
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Biochim. Biophys. Acta 826, 137-146, 1985
A;Title: P31, a mammalian housekeeping protein encoded by a multigene family contains A;Reference number: A15632; MUID:86026347
A;Accession: A15632
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                                                                                                                                      A;Cross-references: GB:X52803; NID:950620; PIDN:CAA36989.1; PID:950621
R;Krummrel, U.; Bang, R.; Schmidtchen, R.; Brune, K.; Bang, H.
FEBS Lett. 371, 47-51, 1995
A;Tile: Cyclophilin-A is a zinc-dependent DNA binding protein in macrophages. A;Reference number: S66416; MUID:95394146
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R;Lad, R.P.; Smith, M.A.; Hilt, D.C.
Brain Res, Mol. Brain Res. 9, 239-244, 1991
A;Title: Molecular cloning and regional distribution of rat brain cyclophilin.
A;Reference number: A60036; MUID:91232390
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A;Residues: 2-21 <KRU>
A;Experimental source: nuclear cyclophilin of H4-7 cells
C;Genetics:
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Pred. No. 0.077;
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A; Reference number: S10327; MUID: 90326555
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A;Residues: 1-164 <LAD>
A;Experimental source: brain
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-164 <DAN>
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                                                                                                                 1-164 <HAS>
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47 GYKGSSFHRII
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submitted to GenBank,
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                                                                                 A; Molecule type: mRNA
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                                                A; Accession: S10327
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peptidylprolyl isomerase (EC 5.2.1.8) A - Chinese hamster
peptidylprolyl isomerase (EC 5.2.1.8) A - Chinese hamster
N'Alternate names: cyclophilin A; cyclosporin A-binding protein A
C; Species: Cricetulus griseus (Chinese hamster)
C; Date: 31 - Mar-1992 fsequence_revision 31-Mar-1992 ftext_change 16-Jul-1999
C; Accession: 807597
R; Bergsma, D.J.: Sylvester, D.
Nucleic Acids Res. 18, 200, 1990
A; Title: A Chinese hamster ovary cyclophilin cDNA sequence.
A; Reference number: 807597; MUD: 90174932
A; Accession: 807597
A; Molecule type: mRNA
A; Residues: 1.164 CBER>
A; Residues: 1.164 CBER>
A; Residues: 1.164 CBER>
C; Cross-references: EMBL:X17105; NID:q49495; PIDN:CAA34961.1; PID:q49496
C; Function:
A; Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
C; Superfamily: peptidylproly isomerase; cyclophilin homology
C; Keywords: cis-trans-isomerase; cyclosporin A binding; T-cell
F; 3-164/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                  peptidylprolyl isomerase (EC 5.2.1.8) - rat (fragments)

peptidylprolyl isomerase (EC 5.2.1.8) - rat (fragments)

peptidylprolyl isomerase (EC 5.2.1.8) - rat (fragments)

peptidylprolyl isomerase (EC 5.2.1.8) - rat (fragments)

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N.Alternate names: cyclophilin A: cyclosporin A-binding protein A
C:Species: Mus musculus (house mouse)
C:Species: Janar-1992 fsequence_revision 31-Mar-1992 ftext_change 16-Jul-1999
C;Accession: S10327; S66416; S40742
R;Hasel, K.W.; Sutcliffe, J.G.
Nucleic Acids Res. 18, 4019, 1990
A:Title: Nucleotide sequence of a cDNA coding for mouse cyclophilin.
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81.8%; Pred. No. 0.064;
1.ve 0; Mismatches 2; Indels
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Pred. No. 0.077;
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72.78;
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            GYKNCTFHRVI 75
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47 GYKGSSFHRII 57
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A; Cross-references: EMBL: Z92784; PIDN: CAB07192.1; GSPDB: GN00019; CESP: F31C3.1
           C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C;Accession: T21587
R;Cottage, A.
R;Cottage, A.
R;Cottage, A.
R;March to the EMBL Data Library, March 1997
A;Reference number: 219446
A;Accession: T21587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: peptidylprolyl isomerase; cyclophilin homology
Keywords: cis-trans-isomerase
28-190/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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Job time: 226 sec
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A; Residues: 1-204 <WIL>
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Best Local Similarity
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A:Introns: 69/3
C:Superfamily: pept
C:Keywords: cis-tre
F:28-190/Domain: cy
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JAGGAGE and ameas: cyclophilin A
C:Species: Pusarium sporotrichioides
C:Species: Pusarium sporotrichioides
C:Species: Pusarium sporotrichioides
C:Species: Pusarium sporotrichioides
C:Accession. J70686; MRN166; J70702
R:Chow. Lp.; UGno. Y: Taugita. A.
Submitted to J7PID, June 1995
A:Reference number: J70686
A:NoCeustion: J70696
A:NoCeustion: J70702
A:NoCeustion: J70702
A:NoCeustion: J70702
A:NoCeustion: Anion acid sequence of peptidyl-prolyl isomerase a of Fusarium sporotrich
A:NoCeustion: Anion acid sequence of peptidyl-prolyl isomerase a of Fusarium sporotrich
A:NoCeustion: J70702
A:NoCeustion: J70702
A:NoCeustion: J70702
A:NoCeustion: J70702
A:NoCeustion: J70702
A:NoCeustion: Anion acid sequence of peptidyl-prolyl isomerase a of Fusarium sporotrich
A:NoCeustion: J70702
A:NoCeustion: Anion acid sequence of peptidyl-prolyl isomerase a of Fusarium sporotrich
A:NoCeustion: J70702
A:NoCeustion: J70702
A:NoCeustion: J70702
A:NoCeustion: Anion acid sequence of peptidyl-prolyl isomerase: Cyclophilin homology
C:Superfamily: peptidylprolyl isomerase: cyclophilin homology
C:Superfamily: peptidylprolyl isomerase specific cPPT>
F:J1970cmant: T710702
C:Superfamily: peptidylprolyl isomerase cyclophilin homology
C:Superfamily: peptidylprolyl isomerase specific cPPT>
F:J2780fiding site: phosphate (Thr) (covalent) (by procein kinase II) **status predicted
F:J2781nding site: phosphate (Thr) (covalent) (by procein kinase II) **status predicted
F:J12781nding site: phosphate (Thr) (covalent) (by cacein kinase II) **status predicted
F:J12781nding site: phosphate (Thr) (covalent) (by cacein kinase II) **status predict
A;Note: the submission to GenBank in entry RATP31 is acknowledged as an unpublished erra
C;Comment: This protein belongs to a class of highly conserved proteins, abundant in thy
                                                                                               *Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Reywords: cis-trans-isomerase; cyclosporin A binding; T-cell F;3-164/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                  80.0%; Score 48; DB 1; Length 164; 72.7%; Pred. No. 0.077; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 48; DB 2; Length 179; 72.7%; Pred. No. 0.084;
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Best Local Similarity 72.7
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GYKNSKFHRVI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity
Matches 8; Conserv
                                                                    C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
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peptidylprolyl isomerase (EC 5.2.1.8) F31C3.1 [similarity] - Caenorhabditis elegans N;Contains: cyclophilin

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Gaps

.; 0

2; Indels

Mismatches

1 GYKNSKFHRVI 11

58 GYKGSSFHRII 68

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RESULT 15 T21587

ö

Gaps ö

Length 204; 2; Indels

Score 48; DB 2; Pred. No. 0.097; 0; Mismatches

80.0%;

us-09-720-469-4.rsp

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January 15, 2002, 13:14:59; Search time 24.88 Seconds (without alignments) 16.210 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                 OM protein - protein search, using sw model
                                                                                                                           Run on:
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US-09-720-469-4 60 1 GYKNSKFHRVI 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39;\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES æ

		Description	P23284 homo sapien	mus m	P80311 bos taurus	homod	echin		P54985 blattella q	_	caenor!	P14851 cricetulus	P17742 mus musculu	P10111 rattus norv	P52013 caenorhabdi	P29117 rattus norv	P30405 homo sapien	neuro		P49792 homo sapien	_	P22011 candida alb	P25007 drosophila	_	P04374 bos taurus	homod		P34790 arabidopsis		Q9qzh3 mus musculu	_		_		
			! ! !																							•									
SUMMAKIES			CYPB_HUMAN	CYPB_MOUSE	CYPB_BOVIN	CYPC_HUMAN	CYPH_ECHGR	CYPB_RAT	CYPH_BLAGE	CYPB_CHICK	CYPB_CAEEL	CYPH_CRILO	CYPH_MOUSE	CYPH_RAT	CYP5_CAEEL	CYPM_RAT	CYPM_HUMAN	CYPH_NEUCR	CYP4_ARATH	RBP2_HUMAN	CYP6_CAEEL	CYPH_CANAL	CYPH_DROME	CYPC_MOUSE	CYPH_BOVIN	CYPH_HUMAN	CYPD_YEAST	CYP1_ARATH	CYPH_CATRO	CYPE_MOUSE	CYPE_DROME	CYPE_HUMAN	CYPH_ALLCE	CYPH_UROFA	PPI_STRCH
		01 :	C	CX	Č	C	C	Č	C	C	C	Ö.	č	č	C	ີວ	Ü	បី	C¥	КВ	Č	Ç	Ç	C	Ç	Ç	Č	Ç	Č	CY	CY	Ç	CY	Ç	Ь
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		Match Length		208	208	212	161	208	164	207	183	163	163	163	204	206	207	223	260	3224	201	162	165	212	163	164	225	172	172	298	300	301	150	163	165
œ	Query	Match	100.0	100.0	91.7	90.0	88.3	86.7	85.0	83	81.7						80.0	80.0	80.0	80.0	78.3	76.7	76.7	76.7	75.0	75.0	75.0	73.3	73.3	73.3	73.3	73.3	71.7	71.7	71.7
		Score	09	09	55	54	53	25	51	20	0.4	<b>3</b>	4.	<b>4</b>	4.	<b>4.</b> 4	20.0	84.	9	84.	4 /	46	46	46	φ. Ω.	4. V		4	4	44	44	4 4	43	43	43
	Result	No.		7	. U.	4 1	ı, n	ا ع	_ `	<b>20</b> (	, נ	9 7	- C	7 .	7 -	4 .	ς;	91	77	87		50	55	22	573	7 C	572	97	7.7	87	53	30	31	32	33

caenorhabdi		_		caenorhabdi	bos taurus	saccharomyc	schizosacch	brassica na	lycopersico	lubinus lut	zea mays (m	
P52010	P52015	P52011	P52009	P52012	P48820	P14832	P18253	P24525	P21568	049886	P21569	
CYP2_CAEEL	CYP7 CAEEL	CYP3_CAEEL	CYP1_CAEEL	CYP4_CAEEL	RBP2_BOVIN	CYPH_YEAST	CYPH_SCHPO	CYPH_BRANA	CYPH_LYCES	CYPH_LUPLU	CYPH_MAIZE	
Н	-	-	٦	-	7	-	-4	-	-1	Н	Н	
171	171	173	192	523	1085	161	162	171	171	172	172	
71.7	71.7	71.7	71.7	71.7	71.7	70.0	70.0	70.0	70.0	70.0	70.0	
43	43	43	43	43	43	42	42	42	42	42	43	
34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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CHAIN
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CYPB_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
RRARY AND DEATH 
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                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-WAR-1992 (Rel. 21, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PEPTIDYL-PROINL GIS-PRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
'X-ray structure of a cyclophilin B/cyclosporin complex: comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         œ.
                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 208 PEPTIDYL-PROLYI, CIS-TRANS ISOMERASE
199 208 PREVENT SECRETION FROM ER.
208 AA; 22742 MW; A814481B7EBD4579 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
Multigene family; 3D-structure.
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0
                          with cyclophilin A and delineation of its calcineurin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 60; DB 1; Length 208; 100.0%; Pred. No. 0.0003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91260697; PubMed-1710767; Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.; "An endoplasmic reticulum-specific cyclophilin."; Mol. Cell. Biol. 11:3484-3491(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M60857; AAA52150.1; -.
EMBL; M63573; AAA36601.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPTISMRASE.
PROSITE; PS00170; CSA_PPIASE_; 1.
PROSITE; PS0072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL;
MEDLINE-92096454; PubMed-1756174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A39118; CSHUB.
PIR; A40515; A40515;
PDB: 17VN: 29-JAN-96
Aarhus/Ghent-2DPAGE, 117; NEPHGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M60457; AAA35733.1;
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 GYKNSKFHRVI 89
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CYPB_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
   SOTT THE STATE OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                      -:- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
-:- SUBCELLUIAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (REL. 32, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
15-UL-1999 (Rel. 38, Last annotation update)
15-UL-1999 (Rel. 38, Last snowERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
16-UL-1995 (RCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
PREVENT SECRETION FROM ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi:
Mammalia; Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea,
ThterPro: IPR00150; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISNRASE.
PROSTE; PS00170; CSA_PPIASE_1; 1.
PROSTE; PS0072; CSA_PPIASE_2; 1.
Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
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                                                                                                                                                                                                                                                       House A.K., Ratajczak T.;
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
488DF5AE40BAD3A7 CRC64;
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MEDLINE-94283623; PubMed-8013656;
Galat A., Bouet F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-NOV-1995 (Rel. 32, Last sequ
15-JUL-1999 (Rel. 38, Last anno
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Carrello A., Mark P.J.,
Submitted (JAN-1993) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208
208
208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P23284; ICYN.
MGD; MGI:97750; Pplb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S21835; S21835.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYPB_BOVIN
P80311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE
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Echinococcus.
                                                                                                                                                                                                                                                                                                                                                    MIM; 123842;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
CYPH_ECHGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P14088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
"Cyclophilin-B is an abundant protein whose conformation is similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
                                                                                                                                                                                                                              -i - CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOBEPTIDES.
-i - FURYINE REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
-i - SUBCELLULAR LOCATION: ENDOPLASHER RETUCHUM LUMEN.
-i - SUBCELLULAR LOCATION: ENDOPLASHER RETICULUM LUMEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schneider H., Charara N., Schmitz R., Wehrli S., Mikol V.,
2urini M.G., Quesniaux V.F., Movva N.R.;
Human cyclophilin C: primary structure, tissue distribution, and
determination of binding specificity for cyclosporins.";
Blochemistry 33:8218-8224(1994).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                   MEDLINE-94280416; PubMed-8010972;
Bose S., Muecke M., Freedman R.B.;
The characterization of a cyclophilin-type peptidyl prolyl cis-trans.isomerase from the endoplasmic-reticulum lumen.";
Blochem. J. 300:871-875(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.7%; Score 55; DB 1; Length 208; 90.9%; Pred. No. 0.0026;
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Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> G (IN REF. 3).
0097C8B289AF6276 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
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MEDLINE*94304830; PubMed=8031755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_lsomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
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26 208 PE
199 208 PR
30 30 K
208 AA; 22701 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D14073; BAA03158.1; -.
                    to cyclophilin-A.";
FEBS Lett. 347:31-36(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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79 GYKDSKFHRVI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P23284; 1CYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYCLOPHILIN C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPIC OR CYPC.
                                                                                   SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYPC_HUMAN
P45877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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RRITH REPRESENTATION OF THE PRICE OF THE PRI
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                   EMBL outstation
                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstatis the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
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01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROUVL GIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lightowlers M.W., Haralambous A., Rickard M.D., \mbox{\tt *Amino} acid sequence homology between cyclophilin and a cDNA-cloned
CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen of Echinococcus granulosus.";
Mol. Biochem. Parasitol. 36:287-290(1989).
-:- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-:- CAPALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
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0
                                                                                                                                   SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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Neodermata; Cestoda; Eucestoda; Cyclophyllidea; Taeniidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54; DB 1; Length 212
Pred. No. 0.0041;
                             PEPTIDE BONDS IN OLIGOPEPTIDES.

-!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CycLosporin; Isomerase; Rotamase; Multigene family.
SEQUENCE 212 AA; 22763 MW; 6F3DB547A2AE581B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR0013130; CSA_PPIBASE.
Pfam; PF00160; pro_isomerase; 1.
PRNUTS; PR00153; CSAPLISHRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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Best Local Similarity
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Gaps

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Indels

Mismatches

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Conservative
                                      1 GYKNSKFHRVI 11
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Matches 9; Conserv
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                                                                79 GYKNSKFHHMI
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6
                                                                                                                                                                                CYPH_BLAGE
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CYPB_CHICK
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  Matches
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-1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPPIDYL-PROINT CIS-TRANS ISOMERASE B PECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92112948; PubMed-1530944;
Arber S., Krause K.-H., Caroni P.;
"S-cyclophilin is retained intracellularly via a unique COOH-terminal
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          œ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOMERASE
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SIGNAL 1 25 RV STATIADETEV
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                                                                                                                                                                                                                                      Score 53; DB 1; Length 161;
Pred. No. 0.0047;
1; Mismatches 1; Indels
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76D12AC3427FEF32 CRC64;
                                                                                                                                                                              161 AA; 17223 MW; 72651E2F4FEF466F CRC64;
                                                                                                                                       208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PROSITE; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                             Pfam; PF00160; pro_isomerase; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90300692; PubMed-2194066; Iwai N., Inagami T.;
                     PIR; A45000; A45000.
HSSP; P05092; 3CYS.
Interpro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kidney Int. 37:1460-1465(1990).
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                                                                                                                                                                                                                                           88.3%;
81.8%;
    EMBL; J04664; AAA29058.1;
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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208
208
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                                                                                                                                                                                                                                                                                                                                              1 GYKNSKFHRVI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYPB_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CYPB_RAT
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Score 52; DB 1; Length 208; Pred. No. 0.0095;

86.7%; 81.8%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- ENZYME RECULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
-I- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- TISSUE SPECIFICITY: UBTOUITOUS.
-i- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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                                                                                                                                                                                     Blattella germanica (German cockroach).
Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Perryota, Neoptera; Orthopteroldea; Dictyoptera; Blattaria;
Blaberoldea; Blattellidae; Blattellinae; Blattella.
NCBI_TaxID=6973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 AA; 17935 MW; A5E25B574DFCDC99 CRC64;
164 AA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 51; DB 1;
Pred. No. 0.011;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 38, Last annotation update)
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          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclosporin; Isomerase; Rotamase.
SEQUENCE 164 AA; 17935 MW; A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                         (Rel. 34, Created)
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             STANDARD;
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47 GYKGSRFHRVI 57
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01-MAR-1992 (
15-JUL-1999 (
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SEQUENCE
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                       SOW WARRAND DRAW DORK TO DORK 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                the secretory pathway.";
J. Biol. Chem. 266:10739-10742(1991).

-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
-!- SUBCELLUTAR LOCATION: EMDOPLASSING RETICULUM LUNEN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
PEPTIDYL-PROLYL CIS-TRANS ISOMBRASE B PRECURSOR (EC 5.2.1.8) (PPIASE) (FOTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP). Gallus gallus (Chicken). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                           MEDLINE-91250364; PubMed-2040593; Caroni P., Rothenfluh A., McGlynn E., Schneider C.; "S-cyclophilin. New member of the cyclophilin family associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pram; PFO0166; pro_isomerase: 1.
PRINTS; PR00153; CSAPPISNRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS0072; CSA_PPIASE_2; 1.
Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
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01-0CT-1996 (Rel. 34, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 11 (EC 5.2.1.8) (PPIASE)
CYP-11 OR T0187.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.3%; Score 50; DB 1; Length 207;
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 AA.
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Rhabditidae; Peloderinae; Caenorhabditis
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MEDLINE-96276416; PubMed-8694762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002130; CSA_PPIase
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207
207
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HSSP; P23284; 1CYN.
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Best Local Similarity
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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P52018;
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01-MOV-1995 (Rel. 32, Last annotation update)
PEPTIDXL-PROJYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN).
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MEDLINE-90174932; Pubmed=2408007;
Marchard D.J., Sylvester D.;
"A Chinese hamster ovary cyclophilin cDNA sequence.";
"A Chinese hamster ovary cyclophilin cDNA sequence.";
"A Chinese hamster correction of PROTEINS.
-!- CHALYTIC ACTIVITY; CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
Page A.P., Macniven K., Hengartner M.O.; "Cloning and blochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans."; Biochem. J. 317:179-185(1996).
                                                                                                                                                                                                                       -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CAPALYIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                       Sims M.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isomerase; Rotamase; Multigene family.
SEQUENCE 183 AA; 20193 MW; 23549C922828C533 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB 1;
Pred. No. 0.03;
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 034955; AAC47115.1; -.
EMBL, 266499; CAA31297.1; -.
HNSP, P05092; 3CYS.
WormPep; T0187.4; CE01588.
InterPro: JPR00130; CSA_PP1ase.
Pfam; PF00160; Pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
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PROSITE; PS50072; CSA_PPIASE_2; 1.
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01-APR-1990 (Rel. 14, Created)
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81.8%;
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Best Local Similarity 81.5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                       SEQUENCE FROM
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INIT_MET
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       SSTTW NO DR R DD R DD R R DD 
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-AuG-1990 (Rel. 15, Last sequence update)
15-DEC-1999 (Rel. 37, Last annotation update)
15-DEC-1999 (Rel. 37, Last annotation SEPEPIDYL-PROIYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN) (SP18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sherry B., farlett N., Strupp A., Cerami A.;
"Identification of gyclophilin as a proinfiammatory secretory product
of lipopolysaccharide-activated macrophages.";
Proc. Natl. Acad. Sci. U.S.A. 89:3511-3515(1992).
-:- FUNCTION: PPLASES ACCELERATE THE FOLDING OF PROFEINS.
-:- CAPALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
-1- SUBCELLULAR LOCKTION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6 X CBA; TISSUE-Thymus; MEDLINE-9032655; PubMed-2197604; Hasel K.W., Sutcliffe J.G.; "Nucleotide sequence of a cDNA coding for mouse cyclophilin."; Nucleic Acids Res. 18:4019-4019(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 1; Length 163;
Pred. No. 0.041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              163 AA; 17768 MW; 02D44F71B8F87A1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 Cyclosporin; Isomerase; Rotamase; Multigene family.
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                                                                                                                                                                                                                                                                                              Pfan: PF00160; pro_isomerase: 1. PRONTS; PROUTS; CSAPPISMRASE PROSITE: PS00170; CSA_PPIASE_1; I. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92228816; PubMed-1565646;
                                                                                                                                                                                                                                                                      Interpro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%;
Similarity 72.7%;
8; Conservative 1
                                                                                                                                                                                                  EMBL; X17105; CAA34961.1; -. PIR; S07597; CSHYAC. HSSP; P05092; 3CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE
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CYPH_MOUSE
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91011; P18303; Occasted)
01-MAR-1989 (Rel. 10, Created)
01-NAR-1989 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROPEIN) (P31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Connern C.P., Halestrap A.P.; "Purification and N-terminal sequencing of peptidyl-prolyl cistrans-isomerase from rat liver mitochondrial matrix reveals the existence of a distinct mitochondrial cyclophilin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and regional distribution of rat brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  17 19 GRV -> TXP (IN REF. 2).
163 AA; 17840 MW; AC724D44DBBF4840 CRC64;
                                                                                                                                                                                                                                                                                                                                                         Cyclosporin; Isomerase; Rotamase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 1;
Pred. No. 0.041;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                             PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
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Lad R.P., Smith M.A., Hilt D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-86026347; PubMed-2996604;
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                                                                                                                                                                    MGD; MGI:97749; Ppia,
InterPro; IPR002130; CSA_PPlase.
Pfam: PF00160; Pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.08;
72.78;
                                                     EMBL; X52803; CAA36989.1; -. P1R; S10327; CSMSA.
                                                                                                                  HSSP; P05092; 3CYS.
SWISS-2DPAGE; P17742; MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA 7:261-267(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cyclophilin."
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MEDLINE=92287042; PubMed=1599421;
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PRINTS; PR00153; CSAPPISMRASE.
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                                                                                                                                                                                                                                                                                                                                                                        80.0%;
                                                                                                                         EMBL; U31948; AAC47126.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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HSSP; P05092; 3CYS.
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Matches 9; Conserv
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                                                                                                                                            P23284;
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                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
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01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 5 (EC 5.2.1.8) (PPIASE) (ROTAWASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Biochem. J. 284:381-385(1992).

-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROTEINS.

-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPHIDES.

-!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF TTS EFFECTS VIA AN IMHIBITORY ACTION ON PPIASE.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC.

-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

-!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page A.P., Macniven K., Hengartner M.O.; "Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans."; Blochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- FUNCTION: PPTASES ACCELERATE THE FOLDING OF PROTEINS.
-1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 AA; 17743 MW; DD16D1C980474414 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyclosporin; Isomerase; Rotamase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.041;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0153; CSAPPISMRASE.
PROSITE; PSO0170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
MEDLINE-96276416: PubMed-8694762;
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PIR; A29819; CSRTA.
HSSP, P05092; 3CYS.
InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M19533; AAA41009.1; -.
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Best Local Similarity 72.77
The 8; Conservative
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SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Connern C.P., Halestrap A.P.;

"Purification and N-terminal sequencing of peptidyl-prolyl cis-trans-
isomerase from rat liver mitochondrial matrix reveals the existence
of a distinct mitochondrial cyclophilin.";

Biochem. J. 284:381-385(1992).

-!- FUNCTION: PRISSES ACCELERATE THE FOLDING OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0BC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 40, Last annotation update)
PEPTIDNI-PROINI. CIST-TANNS ISOMERASE, MITOCHONDRIAL PRECURSOR (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
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Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                      Interpro: IPR002130; CSA_PPIBASE.
Pfam: PF00160; pro_isomerase; 1
PRIMTS; PR00153; CSA_PPIBASE.
PROSITE; PS00170; CSA_PPIASE.1; 1.
PROSITE; PS0072; CSA_PPIASE.2; 1.
ISOMERASE: ROCEMBASE; MILLISERE.2; 1.
ISOMERASE: Z04 AA; 22366 MW; 22ABB39AD1127BAA CRC64;
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MEDLINE-92076192; Pubmed-1744118;
MEDLINE-92076192; Pubmed-1744118;
MEDLINE-92076192; Pubmed-1744118;
Medline D.J., Eder C., Gross M., Kersten H., Sylvester D.,
Appelbaum E., Cusimano D., Livi G.P., McLauglin M.M., Kasyan K.,
Appelbaum E., Cusimano C., Dunnington D., Hand A., Prichett W.P.,
Bossard M.J., Brandt M., Levy M.A.;
The cyclophilin multigene family of peptidyl-prolyl isomerases.
The cyclophilin multigene family of peptidyl-prolyl isomerases.
The cyclophilin multigene family of peptidyl prolyl isomerases.
The cyclophilin multigene family of cyclophilin-itype ppiase Family.
The cyclophilin with the cyclophilin prolyl p
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PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
Cyclosporin: Isomerase; Rotamase; Multigene family; Mitochondrion; Transit peptide.
TRANSIT 1 29 MITOCHONDRION.
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RITOCHONDRION POPERMINALY
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                             PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
MISSING (IN A MINOR FORM).
5 -> R.
C -> A (IN REF. 2).
69048482631B9FAD CRC64;
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30 207 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
207 AA; 22040 MW; D7C76F1D4049F16A CRC64;
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01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 1; Length 206;
Pred. No. 0.053;
0; Mismatches 2; Indels
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Pfam: PP00160; pro_isomerase; 1.
PRORITE; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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206
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21810 A
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Best Local Similarity 81.8
Matches 9; Conservative
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MIM; 604486; -.
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ID CYPM_HUMAN
AC P30405;
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CONFLICT
SEQUENCE
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Query Match 80.0%; Score 48; DB 1; Length 207;
Best Local Similarity 81.8%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GYKNSKFHRVI 11
Db 89 GYKGSTFHRVI 99
Search completed: January 15, 2002, 13:14:59
Job time: 655 sec
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January 15, 2002, 13:16:25; Search time 78:85 Seconds (without alignments) 20.406 Million cell updates/sec
                                                                                                                                                                                                                                                                                                       473505
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                   473505 seqs, 146272329 residues
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Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_vertebrate:*
sp_unclassified:*
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sp_phage:*
sp_plant:*
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sp_bacteria:*
sp_fungi:*
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60
1 GYKNSKFHRVI 11
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Maximum DB seq length: 200000000
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	001490 orpinomyces	088541 rattus norv	Q9bvk5 homo sapien	Q9dcy1 mus musculu	098ue5 xenopus lae	074729 schizosacch	09w227 drosophila	Ogueus plasmodium	027716 plasmodium	O9xzz5 lumbricus r	025093 hirudo medi	O9fw22 orvza sativ	O9r137 mus musculu	O9erb9 mesocricetu	O9u8k2 periplaneta	09n717 leishmanta	_		
SUMMARIES	001490	088541	Q9BVK5	Q9DCY1	Q98UE5	074729	Q9W227	090605	927716	Q9X2Z5	Q25093	Q9FW22	Q9R137	Q9ERB9	Q9U8K2	Q9N717	Q9N0U4	P91791	Q9VUD6
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& Query Match	100.0	100.0	100.0	100.0	90.0	88.3	88.3	85.0	85.0	83.3	81.7	81.7	80.0	80.0	80.0	80.0	80.0	80.0	80.0
Score	09	09	09	9	54	53	53	51	51	20	49	49	48	48	48	48	4.8	48	48
Result No.	-	71	<b>.</b>	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19

095cwj5 mus musculu 01746 brugia mala 023955 dirofilaria 025533 onchocerca 03447 homo sapten 002613 onchocerca 03447 homo sapten 002614 leishmania 095cwj7 mus musculu 09tw32 dictyostell 09tw32 dictyostell 09tw32 dictyostell 09tw32 dictyostell 09tw3 arabidopsis 04tw3 drosophila 044099 drosophila		AA. update) on update) cURSOR (EC 5.2.1.8) (PPIASE) limasticales;	Dbic rumen fungus Orpinomyces errebrate cyclophilin B."; (1995). ING OF PROTEINS.	BY S FAMI	Endoplasmic reticulum.	YL CIS-TRANS ISOMERASE B. AL). STION FROM ER (BY 5BBEC CRC64;
09CWJS 09CZK9 0017246 023955 025633 025633 095184 0943447 095017 095017 095180 099787 099787 099787 099787 099787 099787 099787 099787 099787 099787 099798 099703 099703	ALIGNMENTS	PRT; 203 F Created) Last sequence Last sequence Last noncation Comerase B PREC Incora; Neocall Proces.	8690; L.G.; centric anaerc malogous to ve 92:2587-2591 TRANS ISOMERIZ	PTIDES. SPORIN A (CSA) DOPLASMIC RETI HE CYCLOPHILIN 86.	ase. E. L. L.: L.: Cyclosporin; Endoplasmic	PEPTIDYL-PROLYL CIGCSA (POTENTIAL). PREVENT SECRETION ISIMILARITY). A5748C94305B8BE0
80.0 164 11 80.0 167 11 80.0 171 5 80.0 171 5 80.0 171 5 80.0 177 1 80.0 177 1 80.0 177 1 80.0 259 10 80.0 259 10 80.0 259 10 80.0 259 10 80.0 259 10 80.0 259 10 80.1 259 10		1490 001490 PRELIMINARY; PRT; 203 AA. 001490; CON1490; CLAST CON1490; CON1490; CON1490; CON1490; CON1490; CON1490; CON1490; CON1490; CLAST CON14900; CLAST CON1490; CLAST CON1490; CLAST C	3986; Pubmed=77C 7. L., Ljungdahl In from the poly 7.2 is highly ho 7.2 is highly ho 7.2 is Accellated Paragraphy of Accellated	SOUDS IN OLIGOPE SQULATION: CYCLC JAR LOCATION: EN IY: BELONGS TO T AAD04195.1; ICYN.	(UUZ130; CSA_PPI ) pro_isomerase 153; CSAPPIARAS 170; CSA_PPIASE 170; CSA_PPIASE 170; CSA_PPIASE	23 203 F 447 147 C 200 203 F 53 AA; 21969 MW;
2222 2222 2222 2222 2224 2224 2224 222		1490 001490; 001490; 01-00v-1998; 01-00v	MEDLINE-9522 Chen H., Li ) "A cyclophili sp. strain PC Proc. Natl. A -!- FUNCTION:	-!- ENZYME RE-!- SUBCELLUI -!- SUBCELLUI -!- SIMILAR!! EMBL; U17900; HSSP; P23284; Mendel; 20786	incerpro; 1PF pfam; PF00160 PRINTS; PR001 PROSITE; PS00 PROSITE; PS50 Isomerase; Ro	STUNAL CHAIN BINDING 1 SITE 2 SEQUENCE 20
		OO14 PAC PAC PAC PAC PAC PAT PAT PAT PAT PAT PAT PAT PAT PAT PAC	RX RT RT CC CC	00 <b>00888</b>	7	FT FT SO

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216 AA; 23742 MW; 2D0410A07AA9E420 CRC64;
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                                                                             Ouery Match
Best Local Similarity
Matches 11; Conserv
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Isomerase.
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088541.
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN B (EC 5.2.1.8).
CYCLOPHILIN B (EC 5.2.1.8).
Extrus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i. FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
-i. CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-i. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.
EMBL; AP071225; AAC25590.1; -.
HSSP; P23284; LCYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                      100.0%; Score 60; DB 3; Length 203; 100.0%; Pred. No. 0.0019; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUB-SKIN, AND MELANOMA;
Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; BC001125; AAH01125.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kainer D.B., Doris P.A.; "Cyclophilin B."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 AA; 22802 MW; 02408DFA7157218C CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTINZENOLYL ISOMERASE B (CYCLOPHILIN B).
HOMO Sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db _ 0.0019;
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                                                                                                                                                                                                                                                                        208 AA
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=WISTAR-KYOTO; TISSUE~KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002130; CSA_PPIase.
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                  11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 GYKNSKFHRVI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GYKNSKFHRVI 11
                                                                                                                           1 GYKNSKFHRVI 11
                                                                                                                                                    73 GYKNSKFHRVI 83
                                                           Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCB1_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isomerase;
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                                         Query Match
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Q9BVK5
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STUCENCE FROM TO TAIL STRUCTOREY;

XA STUTE CSTELL GG1: TAISSUE-KIDNEY;

XA ATAKAWA T., Shidata K., Yoshino M., Itoh M., Ishil Y.,

XA ATAKAWA T., Hare A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

XA ATAKAWA T., Hare A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

XA ATAKAWA T., IZAWA M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

XA Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,

XA Schai K., Okido T., Fukuno M., Anon H., Baldarelli R., Barsh G.,

A Sakai K., Okido T., Fukuno M., Anon H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Toyo-oka K., Wang K.H., Weltz C., Whitteker C., Willining L.,

Sasaki H., Toyo-oka K., Wang K.H., Weltz C., Whitteker C., Willining L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                     Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki Y.:
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-69(2001).
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Length 216;
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                                                                     Indels
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PRINTS; PR00153; CSAPDISNRASE.
PROSITE; PS0072; CSA_PP1ASE_2; 1.
SEQUENCE 216 As; 23713 MW; CE9DAD1544AE72FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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100.0%; Score 60; DB 4; L
1larity 100.0%; Pred. No. 0.002;
Conservative 0; Mismatches 0;
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01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002130; CSA_PPIase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, PEPTIDYLPROLYL ISOMERASE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
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PRELIMINARY;
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID-7227;
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                                                                                      CG2852 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                   09W227;
                    09W227
                                                                                                   CG2852
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                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NCV-1998 (TrEMBLrel. 08, Created)
01-NCV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C1709.04C (EC 5.2.1.8).
SPBC1709.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                    SEQUENCE FROM N.A.
Amano T., Yoshizato K.;
*Isolation of genes involved in intestinal remodeling during anuran metamorphosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lyne M., Rajandream M.A., Barrell B.G., Rieger M.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
EMBL, AL031852; CAA2143.1;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDIL-PROLYL CIS-TRANS ISOMERASE B (FRAGMENT).
Xenopus laevis (African clauded frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                     90.0%; Score 54; DB 13; Length 104; 90.9%; Pred. No. 0.012; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 53; DB 3; Length 173; Pred. No. 0.031; l; Mismatches 1; Indels
                                                                                                                                                                          Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF170328; AAK11503.1;
                                                                                                                                                                                                                                104 AA; 11350 MW; 8F6AD1CD1C2FB3E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    il protein; Isomerase; Rotamase.
173 AA: 18905 MW; 116DA3AFSFEUGÖS5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                         173 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISHRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P05092; 2CPL.
InterPro; IPR002130; CSA_PPIase.
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                                                                                                                                                                                                                                                                                    Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                              Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
9; Conserva
                                                                                                                                                                                                                                                                                                                           1 GYKNSKFHRVI 11
                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces
NCBI_TaxID=4896;
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                                                                                            NCBI_TaxID-8355;
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SEQUENCE 17
                                                                                                                                                                                                         somerase
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SEQUENCE
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RA Addams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Randatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Randatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Randano R.C., Rogers Y.-H.C., Blazej R.G., Changen M., Miklos G.L.G., Mandon R.C., Rogers Y.-H.C., Blazej R.G., Changen C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Nalson C.R., Miklos G.L.G., Ballew R.M., Basu A., Baxendall J., Bayerkarogul L., Beasley E.M., Ballew R.M., Basu A., Baxendall J., Bayerkarogul L., Beasley E.M., Ballew R.M., Baulew R.M., Bulley B.M., Ballew R.M., Baulew R.M., Bulley B.M., Burlis K.C., Busam D.A., Buller G., Davengort L.B., Davies P.M., A Gherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.M., A Gherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.M., Burlis K.C., Busam D.A., Buller C., Perraz C., Perriar S., Dunn P., Brosler C., Gabrielian A.E., Garg N.S., Gelbart M.M., Glasser R., Glodek A., Gong F. Gorrell J.H., Gu Z., Galbart M.M., Glasser R., Glodek A., Gong F. Gorrell J.H., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Houston K.A., Howland T.J., Weinrandez J.R., Houston D.L., Alalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Malshina N.Y., Li J.J., Li Z., Liang Y., Lin Z., Liang Y., Lin X., Matteri B., Morfincsh T.C., Morenty C., Morris J., Moshrefi A., Mont S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Reinert K., Nelson K.A., Li J., Li Z., Liang Y., Lin X., Matteri B., Wang Z.-Y., Wassaman D.A., Weilsenbech J., Maring S., Peler E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., Shipen H., Wang Z.-Y., Wassaman D.A., Weilsenbech J., Wang Z.-Y., Wassaman D.A., Weilsenbech J., Wang Z.-Y., Wassaman D.A., Weilsenbech J., Jan Wang Z.-Y., Wassaman D.A., Weilsenbeck G.M., Wang G., Zhu W., Smith H., Shiner K., Zhong W., Zhong G., Zhon W., Zhong G., Zhon W., Zhong G., Zhon W., Shon B.C., Shon H
                                                                                                                                                                                                                                                                                                    Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILEMATIY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERAES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                  Last sequence update)
Last annotation update)
         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; Pubmed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
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HSSP; P23284; ICYN.
FlyBase; FBgn0034753; CG2852.
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MEDLINE-96123383; PubMed-8577319;
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                      Gaps
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Sequence of cyclophilin (cyppfl) gene of Plasmodium falciparum
(isolate FCCI/HN) ";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PEPTIDYL-PROLYC IGS-TRANS ISOMERASES ACCELERATE THE
FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BOUNDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
TRANS_ISOMERASE_FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYL-PROLY CIS-TRANS ISOMERASE PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
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                                                                                                                                                                                                 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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NCBL_TaxID=36329, 57267, 137071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 5; Length 210;
Pred. No. 0.089;
1; Mismatches 1; Indels
DB 5; Length 205
                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 AA; 24049 MW; 778A31CE0FD47D26 CRC64;
                                                                                                                                              Last sequence update)
Last annotation update)
Score 53; DB 5;
Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 AA.
                                                                                                               210 AA
                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                Pfan. PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISNRASE.
PROSITE: PS00170; CSA_PPIASE_1; 1.
PROSITE: PS0072; CSA_PPIASE_2; 1.
PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum (isolate 3D7),
Plasmodium falciparum (isolate Dd2), and
Plasmodium falciparum (isolate hb3).
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                                                                                                                                     Created)
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InterPro; IPR002130; CSA_PPIase.
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81.8%;
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           81.8%;
88.3%;
Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                               PRELIMINARY;
                                                                                                                                                                                       Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isomerase, Rotamase.
SEOUENCE 210 AA;
                                                   1 GYKNSKFHRVI 11
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89 GYKNTTFHRVI 99
                                        1 GYKNSKFHRVI 11
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Best Local Similarity
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SEQUENCE FROM N.A.
STRAIN-FCC1/HN;
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Gaps
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- FUNCTION: PDIASES ACCELERATE THE FOLDING OF PROTEINS.

- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOREPTIDES.

- ENZYME REGULATION: INHIBITED BY CYCLOSPORIN A (CSA).

- INGHEST LEVEL OF EXPRESSION IN ALL ENTYHROCYTIC STAGES, BUT HIGHEST LEVEL OF EXPRESSION IN THE LATE-RING STAGE.
Reddy G.R.; "Cloning and characterization of a Plasmodium falciparum cyclophilin gene that is stage-specifically expressed."; Mol. Blochem. Parasitol. 73:111-122(1995).
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-!- SIMILARIY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.
TRANS ISOMERASE FAMILY.
HESP. PO5091301: CIKL.
INTERPRO 1704.
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Skaryota: Metazoa; Annelida; Clitcilata; Oligochaeta; Haplotaxida;
Lumbricina; Lumbricidae; Lumbricus.
NCBI_TaxID=35632;
                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
MEDLINE-94052193; PubMed-8234327;
Reddy G.R., Chakrabartl D., Schuster S.M., Ferl R.J., Almira B.C.,
Dame J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; PUDDAJ; CALL.
InterPro: IPR002130; CSA_PPIASE.
InterPro: IPR002114; PTS_HPL_SGT.
InterPro: IPR002114; PTS_HPL_SGT.
InterPro: IPR00114; PTS_HPL_SGT.
InterPro: IPR00114; PSP0140; DSA_PPISMSE_1.
IPR0SITE; PS00170; CSA_PPISMSE_1; I.
PROSITE; PS00589; PTS_HPR_SGE; UNCADMASC; SIGNAL
I 39 INTERPROSITE; PS00589; PTS_HPR_SGE; ROLAMASC; SIGNAL
I 39 INTERPROSITE; PS00589; PTS_HPR_SGE; ROLAMASC; SIGNAL
I 30 INTERPROSITE; PS00589; PTS_HPR_SGE; PTS_HPR_SGE; PTS_HPR_SGE; PS00589; PTS_HPR_SGE; PS00589; PTS_HPR_SGE; PS00589; PTS_HPR_SGE; PS00589; PTS_HPR_SGE; PTS_HPR_SGE; PS00589; PTS_HPR_SGE; P
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-!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
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Sturzenbaum S.R., Morgan A.J., Kille P.;
"isolated from earthworms exposed to Cd-supplemented artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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81.8%;
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HSSP; P05092; 2CPL.
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Matches 9; Conservative
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Colgan J.D., Asmal M., Luban J.;
Colgan J.D., Asmal M., Luban J.;
"Haploinentficient growth defects, increased Th2 cytokine production and cyclosporine resistance lacking CyPA.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
HSSP: PO5092: 2CPL.
MGD; MGI:97749; Ppia.
InterPor. IPR002130; CSA_PPIase.
InterPor. IPR002130; CSA_PPIase.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                               SEQUENCE FROM N.A.
Hsing Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M.,
Hsing Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M.,
Hsing Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M.,
Horyza sativa PAC P0015010 genomics sequence, complete sequence.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
By And Shall Shall Shall Seal Processor of Prant PP00160; pro_isomerase.
Prant PP00160; pro_isomerase: I.
PRINTS; PR00153; CSA_PPISMEASE.
PROSITE: PS50072; CSA_PPISME_2; 1.
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murlnae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 10; Length 173; Pred. No. 0.17;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBL_TaxID-4530;
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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81.8%;
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ilarity 72.7%;
Conservative
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Best Local Similarity
9; Conserve
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STRAIN=129/OLA;
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Best Local Similarity
Matches 8; Conserv
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A KOTIMEW S. Blackbhaw S.E., Kaiser K., Davies J.A.;

KOTIMEW S. Blackbhaw S.E., Kaiser K., Davies J.A.;

**CDNA 1lbraries from identified meurons.*;

**I. **CDNA 1lbraries from identified meurons.*;

**Proc. R. Soc. Lond., B. Biol. Sci. 263:57-62(1996).

**PROC. R. Soc. Lond., B. Biol. Sci. 263:57-62(1996).

**POLING OF PROPEIDIS (BY SIMILARITY).

**I. **CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE INIDIC PEPTIDE BONDS IN OLIGORPHIDES.*

**I. **CATALYTIC ACTIVITY: BELOWINGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.*

**PRANS ISOMERASE FAMILY.*

**REMBL: U36797; AAB01531.1; **

**REMBL: PRO0109; PRO_isomerase; I.*

**REMBL: PRO0109; CSA_PPISME_I: I.*

**REMBL: PRO0109; CSA_PPISME_I: I.*

**REMBL: PROSITE: PSO0170; CSA_PPISME_I: I.*

**REMBL: PROSITE: PSO0170; CSA_PPISME_I: I.*

**REMBLE: PSO0170; CSA_PPISME_I: I.*

**REMBLE: PSO0170; CSA_PPISME_I: I.*

**REMBLE: PSO0170; CSA_PPISME_I: I.*

**REMBLE: PSO0170; CSA_PPISME_I: I.*

**REMBL: PROSITE: PSO0170; CSA_PPISME_I: I.*

**REMBLE: PSO0170; CSA_PPISME_I: I.*

**REMBLE: PSO0170; CSA_PPISME_I: I.*
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
SIMILAR TO ARABIDOPSIS THALIANA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (P34791) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Óryza sativa (Rice).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
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0
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81.8%; Pred. No. 0.11;
ive 1; Mismatches 1; Indels
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Pred. No. 0.14;
0; Mismatches 2; Indels
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                                                                                                                                                               164 AA; 17599 MW; B30D22D660966AE7 CRC64;
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Last annotation update)
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                               PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
Pfam; PF00160; pro_isomerase; 1.
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81.88;
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Best Local Similarity 81.ه۰
امری 9; Conservative
                                                                                                                                                                                                                                                           Query Match 83.3
Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                               Isomerase; Rotamase.
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                                                                                                                                                               SEQUENCE
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09FW22
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KITIGHTE P., Bal Y., Li X., Machida C.A.;
Wesocricetus auratus cyclophilin partial cDNA coding sequence.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
TRANS ISOMERASE FAMILY.
TRANS ISOMERASE FAMILY.
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"Isolation of a CDNA sequence encoding a peptidyl-prolyl cis-trans
Submatted (JAW-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PEPTIDYL-PROLYC CIS-TRANS ISOMERASES ACCELERATE THE
FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALYTIC CIS-TRANS ISOMERASES ACCELERATE THE
PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYC CIS-
TRANS, ISOMERASE PAMILY.
                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MON-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMEMSENE (FRGMENT).
Periplaneta americana (American cockroach).
Bukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta: Perrygota: Neoptera; Orthopteroidea; Dictyoptera; Blattaria; NOBL_TAXID-6978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%; Score 48; DB 11; Length 70; 72.7%; Pred. No. 0.11; ive 1; Mismatches 2; Indels
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70 AA; 7841 MW; 472374C1287ACEC9 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                   (Golden hamster).
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Pfam; PF00160; pro_isomerase; 1.
PROSITE; PR00153; CSAPPIANESE.;
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfan; PF00160; pro_isomerase: 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE: PS00170; CSA_PPIASE_1: 1.
PROSITE; PS00170; CSA_PPIASE_2: 1.
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                                       CYCLOPHILIN (FRAGMENT)
                                                                                   Mesocricetus auratus
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NON_TER 1
NON_TER 70
SEQUENCE 70 AA; 71
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                          Mesocricetus.
NCBI_TaxID=10036;
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January 15, 2002, 13:05:28; Search time 81.32 Seconds (Without alignments) 10.020 Million cell updates/sec Run on:

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I NFKLKHYGPGW 11 US-09-720-469-5 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

522463 seqs, 74073290 residues Searched:

522463 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Dat

A_Geneseq_1101:*	1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980	2: /SIDS8/gcgdata/geneseq/genesegp/AA1981	3: /SIDS8/gcgdata/geneseq/genesegp/AA1982	4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983
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| SIDS8/gcdata/geneseq/geneseqp/AA1984\_DAT:
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| SIDS8/gcgdata/geneseq/geneseqp/geneseqp/geneseqp/AA1991\_DAT:
| SIDS8/gcgdata/geneseq/geneseqp/geneseqp/geneseqp/g DAT:\* 9: 10: 11:

/SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT.
/SIDS8/gcgdata/geneseqy/geneseqp/AA1998.DAT.
/SIDS8/gcgdata/geneseqy/geneseqp/AA1999.DAT.
/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT.
/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Human cyclophilin	Human secreted pro	Human cyclophilin	Human cyclophilin	Human cancer assoc	Cyclophilin C. Mu	Human cyclophilin	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia
		·	AAY69925	AAG00090	AAB73302	AAB73301	AAB43878	AAR32353	AAY69947	AAG18027	AAG08983	AAG08982	AAG08981
			21	21	22	22	21	14	21	21	21	21	21
		Match Length DB	11	166	211	216	291	212	10	125	152	204	218
φĐ	Query	Match	100.0	100.0	100.0	100.0	100.0	85.9	83.1	73.2	73.2	73.2	73.2
	•	Score	7.1	7.1	7.1	7.1	71	61	59	52	52	52	52
	Result	No.	1	~	٣	₹	S	9	7	∞	σ	10	11

Arabidopsis thalia		Arabidopsis thalia	Arabidopsis thalla	is	is thali	thali	Arabidopsis thalia	Arabidopsis thalla	ophilin	Human cyclophilin	Arabidopsis thalia	o,	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	s	Arabidopsis thalia	_	Gene 14 human secr	Human secreted pro	Breast cancer-asso	Breast cancer-asso	Breast cancer-asso	Breast cancer-asso	Porcine peptidyl-p		Porcine peptidyl p	Bovine cyclophilin	Cyclophilin. Homo	Calcineurin protei	Human cyclophilin	Human breast cance	Gene 22 human secr
AAG18026	02	AAG44157	AAG44156	AAG44155	AAG29380	AAG29379	AAG05073	AAG05072	AAU01197	AAY69928	AAG15070	AAG48166	AAG15069	AAG48165	AAG16463	AAG16462	AAG16461	AAG76091	AAB64736	AAB64737	AAW44366	AAB98718	AAW44367	AAB98719	AAR10763	AAR72917	AAR72961	AAR13726	AAP90431	AAW56028	AAU01195	AAB98722	AAB51902
21	21	21	21	23	21	21	21	21	22	21	21	21	21	21	21	21	21	22	22	22	19	22	19	22	12	16	16	12	10	13	22	22	21
228	236	9	~	8	0	$\overline{}$	S	S	0	σ	191	192	205	206	252	254	260	82	114	114	121	121	141	141	145	7	145	9	164	9	165	6	301
73.2	73.2										63.4	63.4	63.4	63.4	63.4	63.4						9.09											
52	25	21	51	21	51	21	47	47		45	45	45		45		45	45	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

AAY69925 standard; peptide; 11 AA. 11-APR-2000 (first entry) AAY69925; RESULT AAY69925 

Human cyclophilin B peptide fragment #5.

Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy.

Homo sapiens.

W09967288-A1.

29-DEC-1999.

99WO-JP03360. 24-JUN-1999; 98JP-0178449. 25-JUN-1998;

(SUMU ) SUMITOMO PHARM CO LID. (ITOH/) ITOH K.

Gomi S; Itoh K,

WPI; 2000-116932/10.

Tumour antigen peptides derived from cyclophilin B for treatment and diagnosis of tumours

Claim 4; Page 50; 64pp; Japanese.

us-09-720-469-5.rag

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Page

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Gaps

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Indels

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Mismatches

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11; Conservative

1 NFKLKHYGPGW 11

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Matches
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                                                                                                                                                                                                                                                                                                                    Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or poly4' RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
        This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
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                                                                                                  Score 71; DB 21; Length 11; Pred. No. 9e-06;
                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; SEQ ID 4171; 71pp + CD-ROM; English.
                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                               Human secreted protein, SEQ ID NO: 4171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duclert A,
                                                                                                                                                                                                                           AAG00090 standard; Protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                  gene therapy; chromosome mapping
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                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0122487
                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-500381/45.
                                                                                             Ouery Match
Best Local Similarity
                                                                                                                                               1 NFKLKHYGPGW 11
                                                                                                                                                          1 nfklkhygpgw 11
                                                                 11 AA;
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                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                             EP1033401-A2
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                                                                                                                                                                                                                                                                         06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-2000.
                                                                   Sequence
                                                                                                                                                                                                                                                  AAG00090;
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                                                                                                                                                                                                      RESULT
                                                                                                                                                                    QQ
                                                                                                                                                                                                                                        X0000X8
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Score 71; DB 21; Length 166; Pred. No. 0.00014;

100.0%; 100.0%;

Query Match Best Local Similarity

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The invention relates to a composition for modulating somatolactogenic function, comprising cyclophilin B (Cyple), a mutant of cyclophilin B by particularly a Cyple mutant in which residues 2-12 of the mature protein are absent) or an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone (e.g., prolactin, growth hormone). The invention also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB levels in a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic functions in the animal, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cyclophilin 8 mutant or a composition comprising an inhibitor of the interaction of cyclophilin 8 with a sometolactogenic hormone, is useful for inhibiting sometolactogenic function in the animal. A composition comprising cyclophilin B is useful in the treatment of immunosuppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, is useful for treating HIV infection, breast and prostate cancer, gigantism/aeromegaly, and hyperprolactinemia. The present sequence represents a human cyclophilin B C-terminal mutant, CypB-AIAKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone .
                                                                                                                                                                                                                                                                                                                                                                                                                        Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; glantism; acromegaly; hyperprolactinaemia; C-terminal deletion mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                      Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AlAKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The present sequence is not shown in the specification, but is derived from the wild-type CypB sequence shown on pages 17-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 211;
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Pred. No. 0.00018;
                                                                                         AAB73302 standard; protein; 211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page -; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                             22-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clevenger CV, Rycyzyn MA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-FEB-2001
                                                                                                                                                                         AAB73302;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a composition for modulating somatolactogenic function, comprising eyolophilin B (CypB), a mutant of cyclophilin B (particularly a CypB mutant in which residues 2-12 of the mature protein are absent) or an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone (e.g., prolactin, growth hormone). The invention functions using CypB and a somatolactogenic incomposition in the interaction of somatolactogenic diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB levels in a sample from a patient. Cyclophilin B is unseful for augmenting somatolactogenic functions in the animal, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cyclophilm B mutant or a composition comprising an inhibitor of the interaction of cyclophilm B with a somatolactogenic hormone, is useful for inhibiting somatolactogenic function in the animal. A composition comprising cyclophilm B is useful in the treatment of immunosuppression, in the treatment of short stature, muscle wasting and osteoporosis. Composition comprising cyclophilm B mutant or a composition comprising an inhibitor of the interaction of cyclophilm B with a somatolactogenic hormone, is useful for treating HV infection, breast and prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin
                                                                                                                                                                                                                                                                                                                    Human cyclophilin B: CypB; prolactin-binding; growth hormone-binding; sometolactogenic function modulator; Immunosuppression; short stature; muscle wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; gigantism; acromegaly; hyperprolactinaemia.
      Gaps
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    Indels
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    Mismatches
                                                                                                                                                                  AAB73301 standard; protein; 216 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with somatolactogenic hormone
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                                                                                                                                                                                                                                                                                 Human cyclophilin B (CypB).
                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clevenger CV, Rycyzyn MA;
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11; Conservative
                                                         127 nfklkhygpgw 137
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                                   1 NFKLKHYGPGW 11
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                              22-MAY-2001
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Matches
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include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiathmatic; anticheumatic; antiathritic; antidiametory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, antibodies, antibodies, agonits and antagonists from the present invention may be used to treat immune disorders by activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nuclocides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                                                                                                                                   dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                       diagnosis; cytostatic; proliferative; vulnerary; immunomodulator antidiabetic; antiathatic; antidiabetic; antidiabetic; antidiamatory; antidivid; antiallergic; antibacterial; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or inhibiting the proliferation, differentiation or mobilisation of finunce cells, to treat disorders of hematopoletic cells, autoimmune disorders, allergic reactions, graft versus host discase and organ rejection, modulate haemostatic or thrombolytic activity, modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer - \,
                                                                                                                                                                                                  Human; cancer associated gene; cancer antigen; detection; cancer;
                                                                                                                                                       Human cancer associated protein sequence SEQ ID NO:1323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 1974-1975; 2352pp; English.
                       ¥.
                     AAB43878 standard; Protein; 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2000; 2000WO-US05882.
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                                                                                                         08-FEB-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000.
                                                                AAB43878;
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AAB43878
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Gaps

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Score 71; DB 22; Length 216; Pred. No. 0.00018; 0; Mismatches 0; Indels (

100.08;

Ouery Match 100. Best Local Similarity 100. Matches 11; Conservative

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AAY69947 standard; peptide; 10 AA.
                                                                                                      11-APR-2000 (first entry)
                                                                              AAY69947;
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                           RESULT
AAY69947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A third mammalian cyclophilin, cyp C, was isolated from a CDNA ibrary prepd. from the murine bone marrow derived stronal cell line AC 6. This CDNA was isolated from a substracted sub-library contg. cenes induced by treatment of the stronal cell line with interleuking (IL-1). The message levels for cyp C show a 2-3 fold induction by treatment with IL-1, and this CDNA exhibits a high level of homology with known cyclophilins. Cyp C is distinct from mammalian cyclophilins. Cyp C is distinct from mammalian cyclophilins. Cyp C is distinct from mammalian cyclophilins A and B in both sequence and tissue distribution of expression. A fusion protein contg., e.g. maino acids 16-212 of cyp C possesses peptidyl-prolyl isomerase (PPIase) activity which can be completely inhibited by addition of cyclosporin A (CSA). These cyp C fusion protein of cyclosporin A (CSA). These cyp C intracellular proteins which together form high affinity associations. For example, the cyp C fusion protein binds to a protein of 77 kD in the absence of CSA, while in the presence fo CSA it no longer binds to this p77, but instead binds specifically to a protein of 55 kD, identified as calcineurin (U.S.S.N.07/740175).
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                           Gaps
                                                                                                                                                                                                                                                   Cyclophilin C; bone marrow; stromal cell line; AC 6; interleukin-1; IL-1; cyp A; cyp B; peptidyl-prolyl isomerase; PPIase; cyclosporin A; CsA; ligand; calcineurin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclophilin C polypeptide and nucleic acid encoding it - useful for screening a tissue-specific immunosuppressive agent
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Pred. No. 0.0088;
0; Mismatches 1; Indels
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            Pred. No. 0.00024;
                         Mismatches
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                                                                                                                                             AAR32353 standard; Protein; 212 AA.
100.0%; P1.
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90.9%;
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                                                                                                                                                                                                 (first entry)
                         11; Conservative
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202 nfklkhygpgw 212
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                                                   1 NFKLKHYGPGW 11
          Best Local Similarity
Matches 11; Conserv
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                            Cyclophilin C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour antigen peptides derived from cyclophilin B for treatment and
                                       Cyclophilln B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy.
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ilarity 100.0%; Pred. No. 0.00089;
Conservative 0; Mismatches 0; Indels
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Human cyclophilin B peptide fragment #27
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Matches 9; Conserv
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99US-0142920. 99US-0143977. 99US-014364. 99US-0144005. 99US-0144006. 99US-0144086. 99US-0144086. 99US-0144086.

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99US-0137222.
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990S-0136021.
990S-0136392.
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99US-0134256.
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2000EP-0301439
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99US-0142803
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99US-0151066. 99US-0151080.

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     01 - APR-1999;
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                                                                                                                                                                                                                                                                 DB 21; Length 125;
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Pred. No. 0.17;
1; Mismatches
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                                                      990S-0159294
990S-0159295
990S-01593129
990S-0159313
990S-0159331
990S-0159331
990S-0159638
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99US-0158369.
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Best Local Similarity 81.8%;
Matches 9; Conservative
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99US-0156458
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46 nfklkhtgpgf 56
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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25-0CT-1999;
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PR 19-JUL-1999; 9905 0144331.
PR 19-JUL-1999; 9905 0144331.
PR 19-JUL-1999; 9905 0144331.
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PR 23-AUG-1999; 9905 0153432.
PR 23-AUG-1999; 9905 0153432.
PR 23-AUG-1999; 9905 0153432.
PR 23
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 0.21;
1; Mismatches 1; rodo:
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81.8%;
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23-MAR-1999;
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05-MAR-1999;
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EP1033405-A2
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 1 NFKLKHYGG 10
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Search completed: January 15, 2002, 13:05:28 Job time: 199 sec

Sequence 3 Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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No. 5968802el Nuclear Cyclophilin
21
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HEDIUM TYPE: FIOPPY disk
COMPUTER: TBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: FATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/482.728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION UNMER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1989
TELECOMMUNICATION JORGANICATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ. 10 D. NO: 10:
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US-08-145-995A-11
US-08-451-747-11
US-08-451-134-852-11
S25658-4
US-08-176-500-58
US-08-189-331-58
US-08-471-958-158
US-08-471-958-10
US-08-471-995A-10
US-08-451-747-10
US-08-451-747-10
US-08-451-747-10
US-08-357-598-11
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CITY: San Francisco
STATE: California
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ADDRESSEE: Flehr, Hobbach, Test, Albritton
ADDRESSEE: & Herbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-218-026-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08482728A Patent No. 5968802 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Fisher, Joseph
TITLE OF INVENTION: No. 596
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 amino acids
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ZIP: 94111-4187
  SEOUENCE CHARACTERISTICS
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  LENGTH:
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                                                                                                                                                                                               (without alignments)
6.576 Million cell updates/sec
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Sequence 15,
                                                                                                                                                             January 15, 2002, 13:03:59; Search time 37.64 Seconds
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/GGT2_6/ptodata/2/laa/5B_COMB.pep:*
/GGT2_6/ptodata/2/laa/6A_COMB.pep:*
/GGT2_6/ptodata/2/laa/6B_COMB.pep:*
/GGT2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/GGT2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                                          Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Com
                                                                                                                                                                                                                                                                                                                                                                                                                                                        212252 segs, 22503292 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     sw model
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                                                                                                            - protein search, using
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                        1 NFKLKHYGPGW 11
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Match Length DB
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Gaps

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Length 126;

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Welssman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophiling, Associating Proteins
TITLE OF INVENTION: and Uses
TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61; DB 2; Length 126;
Pred. No. 0.0024;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
ADDRESSEE: Flehr, Hobbach, Test, Albritton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALGALLIA RELEASE #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: PatentIn Policy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08142897
Patent No. 5447852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.9%;
90.9%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 126 amino acids
                                                                    STATE: California
COUNTRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 85.9
Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SS: unknown
unknown
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STATE: California
COUNTRY: USA
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                                       STREET: Four Empored
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                      ADDRESSEE:
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                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissanan, Irving L.
TITLE OF INVENTION: and Uses
TITLE OF INVENTION: and Uses
CORRESPONDERES: 10
CORRESPONDERES: 10
CORRESPONDERES: 10
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08482728A
Patent No. 5968602
GENERAL INFORMATION:
APPLICANT: Fisher, Joseph
APPLICANT: Fisher, Joseph
APPLICANT: Flayen, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATPOINTY AGENT INFORMATION:
NAME: DUDD, Tracy D.
REGISTRATION NUMBER: 34,587
REPRENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELECRAX: 415-326-2400
TELECRAX: 419-326-2402
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                        RESULT 2
US-08-142-897-7
; Sequence 7. Application US/08142897
; Patent No. 5447852
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
COUNTRY: USA
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        70 NFKLKHYGPGW 80
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US-08-482-728A-11
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Gaps ; 0

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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/482,728A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                  CLGASJILCION: ACCUTION: ACCUTION: NAME: SILVA, RODIN M. REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 398-3249
TELER: 910 277299
INFORMATION FOR SEQ ID NO: 11:
E: 8 Herbert
Four Embarcadero Center, Suite 3400
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Gaps

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Indels

Pred. No. 0.79; 0; Mismatches

Mismatches

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GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.0%; Score 44; DB 1; Length 109; 80.0%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   US-08-145-995A-15; Sequence 15, Application US/08145995A; Patent No. 5482850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: RESNICK, DAVID S. REGISTRATION NUMBER: 34235
                    80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 amino acids
                Best Local Similarity 80.0 Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-145-995A-15
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Best Local Similarity
Thas 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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                                                                         1 NFKLKHYGPG 10
                                                                                                 39 NFKEKHTGPG 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 29
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Pred. No. 0.0039;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08482728A
Parent No. 5968802
GENERAL INFORMATION
APPLICANT: Fisher, Joseph
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INTENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
COUNTY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A-61230/DJB/RMS
                                                      NAME: Duon, Tracy D.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
INFORMATION FOR SED ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/482,728A FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/ACENT INPORMATION:
NAME: S11VA, RObin M.
REGISTATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/
TELECOMMUNICATION INFORMATION:
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 777299
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                85.9%;
90.9%;
                                                                                                                                                                                                                                                                                                                                       Query Match 85.9
Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-142-897-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NFKLKHYGIGW 131
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                                                                                                                                                                                                                                                                                                                                                                                                                   1 NFKLKHYGPGW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: unk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-482-728A-12
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TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC TITLE OF INVENTION: COMPOUNDS NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
Sequence 15, Application US/08451747; Patent No. 5821107; GENERAL INFORMATION:
                                                                                 CLOTILDE K.S.
                                                                              APPLICANT: CARLOW, CLOT APPLICANT: PAGE, ANTONY
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64.8%; Score 46; DB 2; Length 126;

Query Match

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Gaps

0;

Pred. No. 1.5; ); Mismatches

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APPLICANT: KEESE, SUSAN
APPLICANT: OBAR, FOOBERT
APPLICANT: WHO YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; · Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,639
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REPERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44;
Pred. No. 1
                       US 08/145,995
                                                                                                                       RECEISTATION NUMBER: 43406
REFERENCE/DOCKET NUMBER: 43406
TELECHOMNICATION INFORMATION:
TELEPHONE: (617) 523-640
TELERA: (617) 523-640
TELEX: 200291 STRE UR
INPORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
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US-08-658-639-13
; Sequence 13, Application US/08658639
; Patent No. 5914238
                                          FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 121 amino acids IYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-658-639-13
                                                                                                                                                                                                                                                                                                                                                            / MOLECULE TYPE: protein US-09-134-852-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NFKLKHYGPG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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  ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-134-652-15
Sequence 15, Application US/09134852
Sequence 15, Application US/09134852
Fatent No. 6127148
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: CARLOW, CLOTILDE K.S.
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC:
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.0%; Score 44; DB 2; Length 109; 80.0%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP. 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTMARE: PC-DOS/MS-DOS
SOFTMARE: PC-DOS/MS-DOS
SOFTMARE: PC-DOS/MS-DOS
SOFTMARE: DC-DOS/MS-DOS
FILLORITON NUMBER: US/09/134,852
FILLORIDON NUMBER: US/09/134,852
CLASSIFICATION:
                                                                                                                                COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: NEB-046-DIV TELECOMMUNICATION: 1FELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
CLASSIFICATION: 514
ATTORREY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-451-747-15
                                                                      STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NFKLKHYGPG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 NFKEKHTGPG 48
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Indels

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RESULT 12
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                                        Gaps
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                                                                                                                                                                                                                                      APPLICANT: KEESEE, SUSAN
APPLICANT: COAR, ROBERT
APPLICANT: WO, YING-JYE
TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurmitz & Thibeault
STREET: 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 121;
     DB 2; Length 121;
                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 5968802el Nuclear Cyclophilin
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/944,604 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION UNBER: 35,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2.4;
60.6%; Score 43; DB
80.0%; Pred. No. 2.4;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/08482728A Patent No. 5968802.
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Fisher, Joseph
TITLE OF INVENTION: No. 5968802e1
                                                                                                                                                                                      Sequence 13, Application US/08944604; Patent No. 6218131; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.68;
80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.6
Best Local Similarity 80.0
Matches 8; Conservative
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-944-604-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
 Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                    1 NFKLKHYGPG 10
                                                                                    1 NFKLKHYGPG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 125 Hi
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02110
                                                                                                                                                                         US-08-944-604-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-08-482-728A-9
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Gaps
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APPLICANT: OBAR, ROBERT
APPLICANT: WI, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 2; Length 127;
Pred. No. 2.5;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: ISBN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,639
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A FILIG DATE: 07-JUN-1995 CLASSIFICATION: 435
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1 Plehr, Hobbach, Test, Albritton
ADDRESSEE: 6 Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                           A-61230/DJB/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 14, Application US/08658639; Patent No. 5914238; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: A-61
TELECOMMINICANTION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
TELEFAX: 910 277299
IMPORATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.6%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 127 amino acids
                                                                         CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-482-728A-9
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-658-639-14
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APPLICANT: Friedman, Jeffrey S. APPLICANT: Welssman, Irving L. TITLE OF INVENTION: No. 5474852el Cyclophilins, Associating Proteins TITLE OF INVENTION: and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                        E: Tracy J. Dunn
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TORNEY AGGS.

NAME: Dunn, Tracy D.

REGISTRATION NUMBER: 34,587
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08145995A
Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
                                                                         RESULT 14
US-08-142-897-8
; Sequence 8, Application US/08142897
; Patent No. 547852
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.68;
                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 80.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: Linear; MOLECULE TYPE: protein US-08-142-897-8
                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          STREET: One Market F
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
    11 111 111
64 NFILKHTGPG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NFKLKHYGPG 10
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                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94105
                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-08-145-995A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: RESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: OBAR, ROBERT
TILLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAT CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
STREET: 125 High St.
                                                                                                                                                                                                                                                                                        DB 2; Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 4; Length 141;
Pred. No. 2.8;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                        Score 43; DB ;
Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/944,604 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08944604 Patent No. 6218131 GENERAL INFORMATION:
REGISTRATION NUMBER: 36,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    60.6%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.6%;
80.0%;
                                                                                                                                LENGTH: 141 amino acids TYPE: amino acid
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-944-604-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                    Query Match .
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                             1 NFKLKHYGPG 10
                                                                                                                                                                                                                                                                                                                                                                                  1 NFKLKHYGPG 10
                                                                                                                                                   TYPE: amino ar STRANDEDNESS: TOPOLOGY: 11m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rry: USA
02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ž
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-944-604-14
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Ouery Match 60.6%; Score 43; DB 1; Length 164; Best Local Similarity 80.0%; Pred. No. 3.3; Matches 8; Conservative 0; Mismatches 2; Indels
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
                                                                                                                       STREET: 130 WAIEN COMMENTY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: BOSTON
ZIP: 02109
ZUP: 02109
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BATENIN PC-DOS/MS-DOS
SOFTWART: PAPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION NUMBER: 34235
ATCASSIFICATION WUMBER: 34235
REFERENCE/DOCKET NUMBER: 3435
REFERENCE/COCKET NUMBER: 3436
TELEFAX: (617) 523-6440
TELEFAX: (617) 623-3400
TELE
```

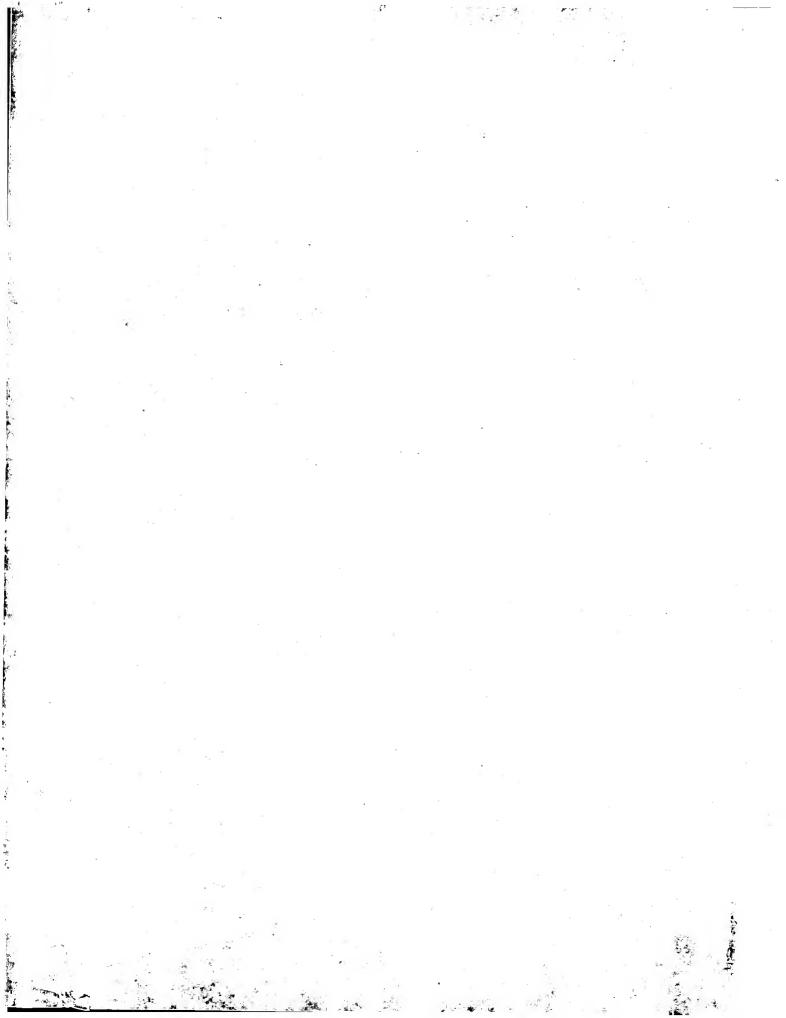
Search completed: January 15, 2002, 13:03:59 Job time: 215 sec

1 NFKLKHYGPG 10 

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0

Gaps ..



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Search time 42.04 Seconds (without alignments) 19.931 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                            January 15, 2002, 13:06:15;
                                                                             OM protein - protein search, using sw model
                                                                                                                       Run on:
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219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 1 NFKLKHYGPGW 11 US-09-720-469-5 Title: Perfect score: Sequence: Scoring table: Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* PIR\_68:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	- 1 "	pertidulorolul iso					. ~	-		peptidylprolyl iso				. –	٠,	vlorolv				peptidylprolyl iso		ā	peptidylprolyl iso	1	peptidylprolyl iso	_			7
	ID	871547	A40516	CSHUB	A56861	T18573	T21587	A40047	A54204	T50838	T49204	T50767	T47724	T50837	T02489	833212	S48018	T18578	863995	868767	A41581	T27034	T52479	B53422	B82777	T27371	T27882	T27373	CSBOAB	CSPGA
	DB	- 2	~	7	7	7	7	7	C	N	~	~	~	~	~		7	7	~	7	~	7	7	7	7	7	7	~	7	<del></del>
	Query Match Length	183	207	208	216	201	204	212	212	204	234	176	176	201	201	573	179	183	164	137	207	192	196	260	350	171	172	173	163	163
œ	Query Match	100.0	100.0	100.0	100.0	94.4	88.7	85.9	85.9		73.2	71.8	71.8	71.8	71.8	0.69	9. 79			64.8	64.8	63.4	63.4	m	63.4	$^{\circ}$	N	62.0	9.09	9.09
	Score	71	7.1	71	7.1	67	63	61	61	52	52	51	51	51	51	49	48	48	47	46	46	45	45	45	45	44	44	44	43	<b>4</b> 3
	Result No.	1	7	3	4	w.	φ.	۲ (	<b>00</b> (	י ייב	01.	T :	12	13	14	12	16	17	18	19	50	21	22	23	24	25	56	27	28	53

peptidylprolyl isomerase (EC 5.2.1.8) (S-cyclophilin) precursor - chicken Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Adria gallus (chicken)
Cispecies: Adria gallus (chicken)
Sizeroni, P. 1. Rothenfluh, A.; McGlynn, E.; Schneider, C.
A;Title: S-cyclophilin. New member of the cyclophilin family associated with the secral A;Title: S-cyclophilin. New member of the cyclophilin family associated with the secral A;Title: S-cyclophilin. New member of the cyclophilin family associated with the secral A;Title: S-cyclophilin New member of the cyclophilin family associated with the secral A;Title: S-cyclophilin New member of the cyclophilin homology
A;Cross-references: GB:MG3553; NID:g212648; PIDN:AAA49064.1; PID:g212649
C;Superfamily: peptidylprolyl isomerase; cyclosponilin homology
C;Neywords: cls-trans-isomerase; cyclosponin A binding
F;34-196/Domain: cyclophilin homology CXPP>

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Gaps ö

0; Indels

Query Match 100.0%; Score 71; DB 2; Length 207; Best Local Similarity 100.0%; Pred. No. 8.9e-05; Matches 11; Conservative 0; Mismatches 0; Indels

peptidylprolyl iso peptidylprolyl iso peptidylprolyl iso peptidylprolyl iso peptidylprolyl iso	peptidylprolyl iso conserved hypothet Ran binding protei peptidylprolyl iso	peptidylprolyl iso cyclophilin (CYP2) peptidylprolyl iso peptidylprolyl iso peptidylprolyl iso	malic acid transpo malic acid transpo asparagine synthet
CSHYAC CSMSA CSRTA CSHTA	S55581 G82517 S58884 T07950	T000/3 E84597 T50772 T12096	В64395 Н64371 Н82255
	- 2 - 2	10000	1000
164 164 165	301 113 3224 172	174 174 248	342 347 554
60.6 60.6 60.6 60.6	59.2	57.7 57.7 57.7 56.3	56.3 56.3
4 4 4 4 4 0 0 0 0 0 0	4 4 4 4 2 4 4 4 4	4444	4 4 4 0 0 0
33 33 33 33 33	35 37 37	339 410 42	444 544

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RESULT

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871547
peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K - rat N:Alternate האחפה: בעירורמים או DDrase
C; Species: Rattus norvegicus (Norway rat)
<pre>C;Date: 15-Nov-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999 C;Accession: S71547</pre>
R;Ruecknagel, K.P.; Pfeifer, T.; Rahfeld, J.U.; Schaerfke, M.; Fischer, G.
submitted to the Protein Sequence Database, November 1996
A; kererence number: S/1547 A; Accession: S/1547
A; Molecule type: protein
A; Residues: 1-183 <rue></rue>
A:Experimental source: liver
C; Superfamily: peptidylprolyl isomerase; cyclophilin homology
C; Keywords: cis-trans-isomerase
F;1-183/Product: peptidylprolyl isomerase, isoform 20.3K #status experimental <pre>cmat&gt;</pre>
F;10-172/Domain: cyclophilin homology <cyp></cyp>
Query Match 100.0%; Score 71; DB 2; Length 183; Best Local Similarity 100.0%; Pred. No. 7:9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NFKLKHYGPGW 11
Db 94 NFKLKHYGPGW 104
RESULT 2
DITORU

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Deptidylprolyl isomerase (EC 5.2.1.8) CyP-S1 precursor - mouse peptidylprolyl isomerase (EC 5.2.1.8) CyP-S1 precursor - mouse (Species: Was musculus (house mouse) (Species: Was musculus (Marchailer 1999) (Species: Was musculus (Marchailer 1999) (Species: Was musculus (Marchailer 1999) (Species: Was musculus (Marchailer 1994) (Marchailer 199
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A; Residues: 9-216 cwork.
A; Cross-references: EMBL:X58990; NID:q53034; PIDN:CAA41736.1; PID:q53035
C; Comment: This protein is distinguished from peptidylprolyl isomerase A by the prese
C; Superfamily: peptidylprolyl isomerase; cyclosportin A binding; endoplasmic reticulum; T-cell
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-216/Product: peptidylprolyl isomerase B fstatus predicted <AMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A. Experimental source: Leratocarcinoma F9 cells
A. Note: sequence extracted from NOB1 backbone (NCBIN:73234, NCBIP:73239)
A.Note: parts of this sequence, including the amino end of the mature protein, were R. Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
R. Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
A. Title: An endoplasmic reticulum-specific cyclophilin.
A. Reference number: A39722; MUID:91260697
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C.Species: Caenorhabditis elegans
C.Sate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C.Accession: T18573; T16351
R.Page, A.P.
Submitted to the EMBL Data Library, May 1995
A.Reference number: 218981
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A;Experimental source: strain N2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: B39722
A,Molecule type: mRnA
A,Residues: 9-216 cule cult.
A) Residues: 9-216 cult.
A) Cross-references: GB:M60456; NID:g192864; PIDN:AAA37498 1; PID:g192865
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A; Description: The sequence of C. elegans cosmid F42G9.
A; Reference number: 218498
A; Accession: T16351
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A:Molecule type: mRNA
A:Residues: 1-201 <PAG>
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A;Reference number: S21835
A;Accession: S21835
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-216 <SCH>
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                                                                                                                                                                                                                                                                                                                  peptidylprolyl isomerase (EC 5.2.1.8) B precursor [validated] - human N.Alternate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin C; Species: Homo sapiens (man) C; Species: 1-Mar-1992 *text_change 08-Dec-2000 C; Accession: A39118; A39722; A40515; S65742 R; Fride, E.R.; Zydowsky, L.D.; Jin, M.; Baker, C.H.; McKeon, F.D.; Walsh, C.T. Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907, 1991 A; Reference number: A39118; MUID:91156714
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A; Residues: 'MiriserN', 1-208 <SPI>A; Residues: 'MiriserN', 1-208 <SPI>A; Residues: 'MiriserN', 1-208 <SPI>A; Note: the authors' translation begins at an ATG codon in poor context for initiation A; Note: the authors' translation begins at an ATG codon in poor context for initiation A; Note: parts of this sequence, including the amino end of the mature form, were confirm R; Mariller, C.; Allain, F.; Kouach, M.; Spik, G.
Biochim. Biophys. Acta 1293, 31-38, 1996
A;Titler, Evidence that human milk isolated cyclophilin B corresponds to a truncated form A; Reference number: S65742; MUID:96186273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:g181250
M.; Maes, P.; Tartar, A.;
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A; Reference number: A39722; MUID:91260697
A; Reference number: A39722; MUID:91260697
A; Accession: A39722
A; Molecule type: mRNA
A; Residues: 1-208 - KHAS>
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A;Tille: A novel secreted cyclophilin-like protein (SCYLP). A;Reference number: A40515; MUID:g1250363
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A,Residues: 26-30;203 <MAR>
A,Experimental source: milk
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                                    1 NFKLKHYGPGW 11
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Best Local Similarity
Matches 11; Conserv
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Length 212:

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R.Jackson, K.; Soll, D.
Mol. Gen. Genet. 262, 830-8, 1999
A.Title: Mutations in a new Arabidopsis cyclophilin disrupt its interaction with prot
A.Reference number: Z22117; MUID:20092489
A.Reference number: T50838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: A54204
R; Schneider, H.; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zurini, M.G.; Quesn Biochemistry 33, 8218-8224, 1994
A; Title: Human cyclophilin C: primary structure, tissue distribution, and determinati A; Reference number: A54204; MUID:94304830
A; Reference number: A54204; MUID:94304830
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A;Experimental source: cultivar Wassilewskija
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 24-Oct-2000
                                                                                                                                                                                                                                                                                                                                                                                                                   peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human
N.Alternate names: cyclophilin C
C.Species: Homo sapiens (man)
C.Spacies: 22-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Experimental source: kidney
A;Note: sequence extracted from NCBI backbone (NCBIN:149387, NCBIP:149388)
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A:Map position: 15421-15422
C.Superfamily: peptidylprolyl isomerase; cyclophilin homology C.Superfamily: peptidylprolyl isomerase; cyclosporin A binding F:37-199/Domain: cyclophilin homology <CYP>
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                                  Score 61; DB 2;
Pred. No. 0.0046;
0; Mismatches 1
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Pred. No.
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81.8%;
                                          85.9%;
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                                                                                                                    10; Conservative
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Best Local Similarity
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Best Local Similarity
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A Molecule type: mRNA
A; Residues: 1-212 <SCH>
                                      Query Match
Best Local Similarity
Matches 10; Conserv
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Cell 66, 799-806, 1991
A;Title: Two cytoplasmic candidates for immunophilin action are revealed by affinity for A;Reference unmber: A40047; WUID:91347379
       A;Cross references: EMBL:U00051; NID:g1216305; PID:g485120; PIDN:AA91355.1; CESP:F42C9.
A;Cross references: EMBL:U00051; NID:g1216305; PID:g485120; PIDN:AA91355.1; CESP:F42C9.
C;Genetics:
A;Genetics:
A;Genetics
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A,Reference number: 21946
A,Recession: T21587
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Rocession: T21587
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Ross-references: EMBL:292784; PIDN:CAB07192.1; GSPDB:GN00019; CESP:F31C3.1
A,Care series: A,Gene: CESP:F31C3.1
A,Rop position: 1
A,Introns: 69/3
C,Superfamily: peptidylprolyl isomerase; cyclophilin homology
C,Reywords: cis-trans-isomerase
F,28-190/Domain: cyclophilin homology <CYP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Contains: Cyclophilin
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C;Accession: T21587
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A;Residues: 1-212 CKRIS
A;Cross-references: GB:M74227; NID:g192898; PIDN:AAA37511.1; PID:g192899
C;Comment: This protein binds the immunosuppressive drug cyclosporin A.
C;Superfamily: peptidylprolyl isomerase: cyclopbilin homology
C;Reywords: cis-trans-isomerase; cyclosporin A binding
F;37-199/Domain: cyclophilin homology CCYP>
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Pred. No. 0.00042;
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Best Local Similarity 90.9
Matches 10; Conservative
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Matches 10; Conserv
A; Residues: 1-201 <TAI>
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Peptidylprolyl isomerase (EC 5.2.1.8) ROC2 - Arabidopsis thailana
N'Alternate names: cytosolic cyclophilin; peptidyl-prolyl cis-trans isomerase; protei
C;Species: Arabidopsis thailana (mouse-ear cress)
C;Date: 20-Apr-2000 *sequence_revision 20-Apr-2000 *text_change 21-Jul-2000
C;Accession: T47724; S71220
R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K. A;Reference number: 224474
A;Reference number: 224474
A;Status: preliminary
A;Notcession: T47724
A;Status: preliminary
A;References: EMBL:ArF18021
A;Experimental source: cultivar Columbia; BAC clone F18021
R;Chou. I.T.; Gasser, C.S.
Submitted to the EMBL Data Library, November 1995
A;Description: Characterization of cyclophilin gene family in Arabidopsis thaliana.
A;Reference number: S71219
A;Reference number: S71219
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A. Reference number: 225256; MUID:99205703
A. Reference number: 225256; MUID:99205703
A. Residues: 1-201 csal.>
A. Residues: 1-201 csal.>
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A. Residues: 1-201 csal.>
A. Reperimental source: Landsberg erecta
C. Genetics:
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A; Residues: 1-171.'N', 173-176 <CHO>
A; Cross-references: EMBL:U40400; NID:g1305456; PIDN:AAB96813.1; PID:g1305457
C; Genetics:
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A. Note: P18021.30
C.Superfamily: peptidylprolyl isomerase: cyclophillin homology
C.Keywords: Cis-trans-isomerase, cyclosporin A binding
F.3-171/Domain: cyclophilin homology cCYP>
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C:Superfamily: peptidylprolyl isomerase: cyclophilin homology
C:Keywords: cis-trans-isomerase
F:31-199/Domain: cyclophilin homology <CYP>
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90.0%; Pred. No. 0.22;
iive 0; Mismatches
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Pred. No. 0.2;
0; Mismatches
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Best Local Similarity 90.0°
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A Molecule type: DNA
A Residues: 1-234 <BEN>
A REAGleus: 1-234 <BEN>
A COSS-references: EMBL:AL163832; GSPDB:GN00061; ATSP:P27K19.100
A EXPERIMENTAL SOURCE: Cultivar Columbia; BAC clone F27K19
A Genetics:
A Gene: ATSP:F27K19.100
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      Mismatches
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81.8%; Pred. No. 0.17
tive 1; Mismatches
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                                                                                       125 NFKLKHTGPGF 135
                                                      1 NFKLKHYGPGW 11
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peptidylproly1 isomerase (EC 5.2.1.8) F23F1.12 - Arabidopsis thaliana
NiAternate names: cyclophilin; protein At2g29960; protein F23F1.12
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crospy, M.L.; Brandon, R.C.; Sykes, S.M.; Kaull
A;Residues: 17031 #SROUN
A;Reference and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: 844420; MUID:20083487
A;Residues: 027 #SROUN
A;Recession: 684702
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C. Species: Trichoderma harzianum
R. Vasseur, V.V.: van Montagu, M.M.: Goldman, G.G.H.
R. Vasseur, V.V.: van Montagu, M.M.: Goldman, G.G.H.
A. Description: Molecular Characterization of mycoparasitic-related genes of Trichoderma A. Reference number: S33212
A. A. Cocession: S33212
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A;Molecule type: DNA
A;Molecule 19: 2014 CSTO
A;Residues: 1-201 CSTO
A;Cross-references: GB:AE002093; NID:g3420055; PIDN:AAC31856.1; GSPDB:GN00139
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A;Nolecule type: DNA
A;Nolecule type: DNA
A;Residues: 1-573 <VAS>
A;Residues: 1-573 <VAS>
A;Residues: B;Nolecule type: DNA
C;Superfamily: arginine permease
C;Superfamily: arginine permease
C;Reywords: amino acid transport; glycoprotein; transmembrane protein
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A;hatrons: 22/3; 46/1; 62/1; 70/1; 131/1
A;Note: P23F1.12
C;Superfamily: peptldylprolyl isomerase; cyclophilin homology
C;Superfamily: peptladylprolyl isomerase; cyclosporin A binding
F;31-199/Pomain: cyclophilin homology <CYP>
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                                              122 NFKLKHTGPG 131
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein · protein search, using sw model

Run on:

January 15, 2002, 13:14:59; Search time 24.88 Seconds (Without alignments) 16.210 Million cell updates/sec

US-09-720-469-5 71 1 NFKEKHYGPGW 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	P24367 gallus gall	311 bos tas	homod	mus T	P24368 rattus norv	_	-		_		P52018 caenorhabdi	P54985 blattella q					P52010 caenorhabdi	-	P52011 caenorhabdi	P04374 bos taurus	cric			P05092 homo sapien	_	Q9unp9 homo sapien		P49792 homo sapien	P34790 arabidopsis	_	_		
	ID		CYPB_BOVIN	CYPB_HUMAN	CYPB_MOUSE	CYPB_RAT	CYP6_CAEEL	CYP5_CAEEL	CYPC_HUMAN	CYPC_MOUSE	INA1_TRIHA	CYPB_CAEEL	CYPH_BLAGE	CYPM_RAT	CYPM_HUMAN	CYP1_CAEEL	CYP4_ARATH	CYP2_CAEEL	CYP7_CAEEL	CYP3_CAEEL	CYPH_BOVIN	CYPH_CRILO	CYPH_MOUSE	CYPH_RAT	CYPH_HUMAN	CYPE_MOUSE	CYPE_HUMAN	RBP2_BOVIN	RBP2_HUMAN	CYP1_ARATH	CYPB_VICFA	Y762_METJA	Y576_METJA	ASNS_SANAU
	Length DB	207 1	208 1	208 1	208 1	208 1	201 1	204 1	212 1							192 1																		524 1
4	Match	100.0	100.0	100.0	100.0	100.0	94.4	88.7	85.9	85.9	0.69	9.79	66.2	64.8	64.8	63.4	63.4	62.0	62.0	62.0	9.09	9.09	9.09	9.09	9.09	9.09	9.09	27.7	59.2	57.7	57.7	56.3	56.3	56.3
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Ouery Match 100.0%; Score 71; DB 1; Length 207; Best Local Similarity 100.0%; Pred. No. 3.6e-05; Matches 11; Conservative 0; Mismatches 0; Indels

22413 MW;

207 AA;

SEQUENCE

DR DR WW KW FT FT FT SO SO

BY SIMILARITY.
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE I
PREVNT SECRETION PROM ER
(BY SIMILARITY).
D9COC2E528E25559 CRC64;

P49092 lotus japon P19251 pisum sativ P49093 lotus japon O24661 triphysaria P31752 asparagus o Q9u3v9 drosophila P1952 pisum sativ P57923 pasteurella P4327 haemophilus P23615 saccharomyc	PRESILT 1  TO PARALLE STANDARD; PRT; 207 AA.  TO PAJ 167.  TO 1-MAR-1992 (Rel. 21, Created)  TO 1-MAR-1992 (Rel. 21, Created)  TO 1-MAR-1992 (Rel. 21, Last sequence update)  TO 1-MAR-1992 (Rel. 22, Last sequence update)  TO 1-MAR-1992 (Rel. 23, Last sequence update)  TO 1-MAR-1992 (Rel. 23, Last sequence update)  TO 1-MAR-1992 (Rel. 23, Last sequence update)  REGALON (COLORADIA)  TO 1-MAR-1992 (Rel. 23, Last sequence update)  TO 1-MAR-1992 (Rel. 23, Last sequence update)  TO 1-MAR-1992 (Rel. 23, Last sequence update)  TO 2-MAR-1992 (Rel. 23, Last sequence update)  TO 3-MAR-1992 (Rel. 23, Last sequence update)  TO 4-MAR-1992 (Rel. 1992)  TO 4-MAR-1992 (Rel. 1992)  TO 4-MAR-1992 (Rel. 1992)  TO 5-CO-POPILIA (Rel. 1992)  TO 7-MAR-1992 (Rel. 1992)  TO 8-MAR-1992 (Rel. 1992)  TO 8-MAR-1992 (Rel. 1992)  TO 7-MAR-1992 (Rel. 1992)  TO 7-MAR-1992 (Rel. 1992)  TO 8-MAR-1992 (Rel. 1992)  TO 8-MAR-1
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33 585 1 585 1 585 1 585 1 585 1 585 1 585 1 585 1 595	STANDARD;  11. 21, Create 11. 38, Last s.  11. 38, Last s.  12. Create 11. 38, Last s.  13. Cristrans 15  13. Cristrans 15  14. PubMed=204  44. PubMed=204  44. PubMed=204  44. PubMed=204  66. Hub A., Mc  New member s.  11. A. PubMed=204  11. Cristrans s.  12. Cristrans s.  13. Cristrans s.  14. Cristrans s.  15. Cristrans s.  16. Cristrans s.  17. Cristrans s.  18. Cristrans s.  18. Cristrans s.  19. Cristrans s.  19. Cristrans s.  19. Cristrans s.  10. Cris
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	CHCRE CYPBECHICK STANDARI CYPBECHICK STANDARI D194367; D1-MAR-1992 (Rel. 21, 01) D1-JUL-1999 (Rel. 38, 12) CROTAMASE) (CRIC. 21, 13, 13) CROTAMASE) (CYCLOPHILI) GALIUS (GALIUS (GALICA) REDATASE) (CYCLOPHILI) CATCHOSAUTIA; AVES: NEOG ARCHOSAUTIA; AVES: NEOG
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Pred. No. 3.6e-05; Mismatches 0:

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                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
11-NUL-1999 (Rel. 38, Last annotation update)
12-NUL-1999 (Rel. 38, Last annotation update)
12-NUL-1999 (Rel. 38, Last annotation update)
13-NUL-1909 (Rel. 32, Last annotation update)
13-NUL-1909 (Rel. 38, Last annotation u
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOSE S., Muccke M., Freedman R.B.;
"The characterization of a cyclophilin-type peptidyl prolyl
cis-trans-isomerase from the endoplasmic-reticulum lumen.";
Blochem. J. 300:871-875(1994).
-ir FUNCTION: PPIASES ACCEREATE THE FOLDING OF PROTEINS.
-ir CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
-ir SUBGRIGATION: CYCLOSPORTNA A (CSA) INHIBITS CYPB.
-ir SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-ir SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-ir SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carrello A., Mark P.J., House A.K., Ratajczak T.;
Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
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Pfam; PF00160; pro_isomerase; 1.
PRNINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 26-45.
MEDLINE-94280416; PubMed-8010972;
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22701 MW;
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                                                                                                                                                                                                                                         STANDARD;
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P80311;
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Length 208;

DB 1;

Score 71;

100.08;

Query Match

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01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1991 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-51).
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Arber S., Krause K.-H., Caronl P.;
"S-cyclophilin is retained intracellularly via a unique COOH-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl isomerase with a signal sequence.";
Proc. Natl. Acad. Sci. U.S.A. 88:1903-1907(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microsequences of 145 proteins recorded in the two-dimensional gel
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-i- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-i- CATALAIL ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC.
PEPTIDE BONDS IN OLICOPEPTIDES.
-i- ENLYME RECULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
-i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelcostomi;
Mammalia; Eutheria; Primates; Catarnhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. BubMed=2040592;
SEQUENCE FROM N.A. BubMed=2040592;
Spik G., Haendler B., Delmas O., Mariller C., Chamoux M., Maes is Tartar A., Montreull J., Stedman K., Kocher H.P., Keller R., Tartar A., Montreull J., Stedman K., Rocher H.P., Keller R., Tartar A., Move N.R.;
Tartar A. Movel Secreted cyclophilln-like protein (SCYLP).";
J. Biol. Chem. 266:10735-10738(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94255495; PubMed-8197205; , MIKOL V. Kallen J., Walkinshaw M.D.; Mixot V. Kallen J., Walkinshaw M.D.; Mixray structure of a cyclophilin B/cyclosporin complex: comparth cyclophilin A and delineation of its calcineurin-binding domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rasmussen H.H., van Damme J., Puype M., Gesser B., Cells J.E. Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 26-40.
MEDLINE-91156714; PubMed-2000394;
Price E.R., Zydowsky L.D., Jin M., Hunter C.H., McKeon F.D.,
Walsh C.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence and colocalizes with the calcium storage protein calreticulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 2-208 FROM N.A. MEDLINE-91260697; PubMed-1710767; Assal K.W., Glass J.R., Godbout M., Sutcliffe J.G.; Hasel K.W., Specific cyclophilin."; Mol. Cell. Biol. 11:3484-3491(1991).
                                                                                                                                                                                                         208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
                                                                                                                                                                                                         PRT;
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100.08; Pre-
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                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION.
                                                                                               119 NFKLKHYGPGW 129
                                                                        1 NFKLKHYGPGW 11
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                            PPIB OR CYPB.
                                                                                                                                                                                                           CYPB_HUMAN
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SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22713 MW;
                                                                                                                                                                                                                          EMBL; M60456; AAA37498.1; -. EMBL; X58990; CAA41736.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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208
208
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PIR; S21835; S21835.
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                    HSSP; P23284; 1CYN.
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           STTTT WERE BORRED BREEF TO SOUTH STREET TO SOU
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                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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1-WAR-1992 (Rel. 21, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PEPTIDYL-PROMYL GIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
[EQTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS PRO0160; pro_isconerase; 1.
PRINTS PRO0153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPISME_1; 1.
PROSITE; PS00170; CSA_PPISME_2; 1.
Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Miltigene family; 3D-structure.
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- 1 - SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 71; DB 1; I 100.0%; Pred. No. 3.6e-05;
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                                                                                                                                                                                                                                        EMBL; M63573; AAA36601.1; ALT_INIT.
EMBL; M60457; AAA35733.1; -.
                                                                                                                                                                                                                                                                                                                                                Aarhus/Ghent-2DPAGE; 117; NEPHGE.
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002130; CSA_PPIase
                                                                                                                                                                                                                   EMBL; M60857; AAA52150.1; -.
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Best Local Similarity 100.
Matches 11; Conservative
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208
208
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PIR; A40515; A40515.
PDB; 1CYN; 29-JAN-96.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                        MIM; 123841;
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P24369;
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01-WAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROMYL GIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAWASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
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-1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutherla; Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B. PREVENT SECRETION FROM ER
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J. Cell Biol. 116:113-125(1992).
J. FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iwai N., Inagami T.;
*Molecular cloning of a complementary DNA to rat cyclophilin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
SIGNAL 1 25 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 71; DB 1; Length 208; 100.0%; Pred. No. 3.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY),
4BBDF5AE40BAD3A7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
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                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                      MGD; MGI:97750; Ppib.
InterPro; IPR002130; CSA_PPIase.
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POTENTIAL.
PETITIVIL-PROLYL CIS-TRANS ISOMERASE 6.
N-LINKED (GLCNAC. . .) (POTENTIAL).

-LINKED (GLCNAC. . .) (PO 084C5762917F958B CRC64;

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PROSITE; PS50072; CSA_PPLASE_2; 1,
ISOMETASE; Rotamase; Multigene family; Signal.
SIGNAL 1 16
                                                                                                           201 AA; 21864 MW;
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P52013;
                                                                                      CARBOHYD
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                                              SIGNAL
                                                                     CHAIN
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1-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 6 PRECURSOR (EC 5.2.1.8) (PPIASE)
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALVITC SIS-TRAND ISOMERIZATION OF PROLINE IMDIC PEPTIDE BONDS IN OLICOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                      ISOMERASE
                       HSSP; P23284; ICYN.
Interpro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS05072; CSA_PPIASE_2; 1.
Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
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      SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY
                                                                                                                                                                                                                                                                                                                                                 Length 208;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
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PREVENT SECRETION FROM ER
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 71; DB 1; I
100.0%; Pred. No. 3.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
MEDLINE-96276416; Pubmed-8694762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wormbep; F4269.2; CE01301.
InterPro: IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase: 1.
PRIMTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                                                                                                                                     23025 MW;
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CYP-6 OR F42C9.2.
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HSSP; P23284; 1CYN.
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                               25
208
208
                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 NFKLKHYGPGW 129
                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NFKLKHYGPGW 11
                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYP6_CAEEL
P52014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            raich A.;
                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                   SIGNAL
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01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIOYL-PROLIL CIS-TRANS ISOMERASE 5 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorca; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page A.P., Macniven K., Hengartner M.O.;
"Cloning and blochemical characterization of the cyclophilin
homologues from the free-living nematode Cgenorhabditis elegans.";
Blochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-:- CATALYTIC SCATIVITY: CIS-TRAND ISOMERIZATION OF PROLINE IMIDIC
-:- STATIOE BONDS IN OLIGOPEPTIDES.
-:- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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   Length 201;
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                                                             Indels
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Pfam: PF00160; Pro_Leomerase: 1.
PROSITE: PS00170; CSA_PPIASE_1: 1.
PROSITE: PS00770; CSA_PPIASE_1: 1.
PROSITE: PS00770; CSA_PPIASE_2: 1.
ISOMERASE: ROLfamase: Multigene family.
SEQUENCE 204 AA: 22366 WW: 22ABB39AD1127BAA CRC64;
Score 67; DB 1; Le
Pred. No. 0.00017;
1; Mismatches 0;
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90.9%; Pred. No. 0.00082;
                                                                                                                                                                                                                                                                                                                        204 AA.
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                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
MEDLINE-96276416; Pubmed-8694762;
      94.4%;
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Matches 10; Conservative
                                                             Conservative
                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans
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                                                                                                                                                                             109 NFKLOHYGPGW 119
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                                                                                                                     1 NFKLKHYGPGW 11
                              Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CYCLOPHILIN-5).
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MEDLINE=91347379; PubMed=1652374;
                                       absence of CsA.";
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                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P30412;
01-APR-1993 (Rel. 25, Created)
01-NPR-1993 (Rel. 25, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAWASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.9%; Score 61; DB 1; Length 212; 90.9%; Pred. No. 0.0019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclosporin, Isomerase, Rotamase, Multigene family.
SEQUENCE 212 AA; 22763 MW; 6F3DB547A2AE581B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
       PRT;
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PROSITE; PSOOJ70; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00160; pro_isomerase; 1.
                                                                                                                                                                                                                                                                                                                                                                                  InterPro, IPR002130; CSA_PPIase
                                                                                                                                                                                                                                                                                                                                                      EMBL; S71018; AAB31350.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 85.9
Best Local Similarity 90.9
Matches 10; Conservative
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      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NFKLKHYGIGW 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NFKLKHYGPGW 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CYCLOPHILIN C).
PPIC OR CYPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-10090;
                                                                                                               NCBI_TaxID=9606;
                                                                        PPIC OR CYPC.
                       01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                       MIM; 123842;
     CYPC_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYPC_MOUSE
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CYPC_MOUSE
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Friedman J., Weissman I.L.; "Two cytoplasmic candidates for immunophilin action are revealed by affinity for a new cyclophilin; one in the presence and one in the
                                                                                                                         Cell 66:799-806(1991).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
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MEDLINE-95291429; PubMed-7773384;
Vasseur V.V., van Montagu M.M., Goldman G.G.H.;
"Trichoderma harzianum genes induced during growth on Rhizoctonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Trichoderma.
NCBL_TaxID-5544;
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                                                                                                                                                                                                                                                           -:- ENTYME REGULATION: CYCLÓSPORIN A (CSA) INHIBITS CYPC.
-:- SUBCELLULAR LOCATION: CYTOPLASMIC.
-:- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclosporin; Isomerase; Rotamase; Multigene family.
SEQUENCE 212 AA: 22794 MW; C99E7AA5D0FA04B6 CRC64;
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- INDUCTION: DURING MYCOPARASITISM.
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01-FEB-1994 (Rel. 28, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
MMINO-ACID PERMEASE INDAL.
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HSSP; P05092; 2RMC.
MGD; MGI:97751; Ppic.
InterPro; 1PR00130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSA_PFIASASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_2; 1.
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Best Local Similarity 90.9
Matches 10; Conservative
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EMBL; Z66499; CAA91297.1; -.
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SEOUENCE 16
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P54985;
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page A.P., Macniven K., Hengartner M.O.; "Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans."; Blochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PPIASES ACCEBRATE THE FOLDING OF PROTEINS.
-!- CATALITIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
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                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPIIOYL-PROLY CIS-TRANS ISOMERASE 11 (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCHOFHILIN-11).
                                                                                                                                                                                                                                           Score 49; DB 1; Length 573;
Pred. No. 0.55;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                              5FB0A806934DB55D CRC64;
                                                                                  Transport; Amino-acid transport; Transmembrane. TRANSMEM 72 92 POTENTIAL.
                                                                                                                                                                                                                                                        ed. No. 0.55;
Mismatches
                                                                                                                                                                                                                                                                                                                                                               183 AA.
                                       InterPro; IPR002293; AA_rel_permease_1.
InterPro; IPR002027; Amino_acid_permease.
Pfam: PF00324; aa_permeases; IPR0021E; PS00218; AMINO_ACID_PERMEASE_1; 1.
                                                                                                                           POTENTIAL.
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MEDLINE-96276416; PubMed-8694762;
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80.0%;
                   EMBL; 222594; CAA80308.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U34955; AAC47115.1; -
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                                                                                                                                                                                                                                                                  Conservative
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200
229
229
280
315
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                                                                                                                                                                                                                                  Query Match
Best Local Similarity
8; Conserve
                                                                                                                                                                                                                                                                                       1 NFKLKHYGPG 10
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabdit
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P52018;
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MEDLINE-96096751; PUDMed-8529654;

MEDLINE-96096751; PUDMed-8529654;

A MATTINE-96096751; PUDMed-8529654;

A MATTINE-96096751; PUDMed-8529654;

A MATTINE-96096751; PUDMed-8529654;

T "Characterization of a cDNA encoding a cytosolic peptidylprolyl cistrans isomerase from Blattella germanica.";

Eur. J. Biochem. 234.284-292(1995).

- I EUR. J. Biochem. 234.284-292(1995).

- THORTION: PPINSES ACELERATE THE FOLDING OF PROFEINS.

- TOTALXTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.

- PETIDE BONDS IN CHOPPINS ACTION ON PPIASE.

- TISSUE SPECIFICITY: UBICOUTOUS.

- I TISSUE SPECIFICITY: UBICOUTOUS.

- I SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
PEPTIDYL-PROINL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta
Blerryota: Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea: Blatteilidae; Blatteilinae; Blatteila.
NCBL_TaxID=6973;
                                                                                                                                                                                                                                                                                                                                                                             Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                              Isomerase; Rotamase; Multigene family.
SEQUENCE 183 AA; 20193 MW; 23549C922828C533 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 AA; 17935 MW; ASE25B574DFCDC99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 1;
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blattella germanica (German cockroach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
WormPep; T0187, 4; CE03588.
InterPro: IPR002130; CSA_PPlase.
Ffam; PF00160; pro_isomerase; 1.
PRONTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002130; CSA_PPIase, Pfam; PF00160; pro_isomerase; 1. PRINTS; PK00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                                                                                                             67.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 NFELKHIGPG 114
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NFKLKHYGPG 10
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Length 164;

Score 47; DB 1; Pred. No. 0.36;

66.2%; 80.0%;

128 NFTLKHVGPG 137

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Gaps

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Indels

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Mismatches

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Conservative

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Matches

1 NFKLKHYGPG 10

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                                                                                                                                                                                                                                                                                                                                                                                                **MEDLINE-92078192; PubMed-1744118; MEDLINE-92078192; PubMed-1744118; MEDLINE-92078192; PubMed-1744118; MEDLINE-92078192; PubMed-1744118; Mersten H., Sylvester D., A Appelbaum E., Cusimano D., Livi G.P., McLauglin M.M., Kasyan K., Porter T.G., Silverman C., Dunnington D., Hand A., Prichett W.P., Bossard M.J., Brandt M., Levy M.A.; The cyclophilin multigene family of peptidyl-prolyl isomerases. T. The cyclophilin multigene family of peptidyl-prolyl isomerases. T. Biol. Chem. 266:23204-23214(1991).

C. -: FUNCTION: PPIASES ACCEREATE THE FOLDING OF PROTEINS.

C. -: CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDES.

C. -: SUBCELLULAR LOCATION: MITCHONBRIAL MATRIX.

C. -: SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyclosporin; Isomerase; Rotamase; Multigene family; Mitochondrion;
                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDYE-PROLYL CIS-TRANS ISOMERASE.
D7C76F1D4049F16A CRC64;
                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-FUDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONRIAL PRECURSOR
(EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MITOCHONDRION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 1;
Pred. No. 0.67;
); Mismatches
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(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
                                    207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro: IPR00130; CSA_PPIase.
Pfam: PF00160; pro_isomerase; 1.
PRNUTS: PR00150; CSAPISMRASE.
PROSITE: PS00170; CSA_PPIASE_1: 1.
PROSITE: PS50072; CSA_PPIASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22040 MW;
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80.0%;
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                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A41581; A41581.
HSSP; P05092; 3CYS.
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Best Local Similarity
Matches 8; Conserv
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01-0CT-1996
20-AUG-2001
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P52009;
                                       CYPM_HUMAN
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CYP1_CAEEL
      CYPM_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
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                                                                DATE THE REAL PROPERTY OF THE 
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SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDYL-PROLYL CIS-TRANS ISOMERASE. MISSING (IN A MINOR FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                           01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROUL CIS-TRANS ISOMERASE, MITOCHONORIAL PRECURSOR (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN F).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Price N.T., Woodfield K.Y., Halestrap A.P.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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69048482631B9FAD CRC64;
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                                                                                                                                                206 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-WISTAR; TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP: P05092; 3CYS.
InterPro; IPR002130; CSA_PPIase.
Pfan, PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSA_PPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_1; 1.
                                                                                                                                                   PRT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92287042; PubMed-1599421;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U68544; AAB08453.1; -.
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80.0%;
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206
39
31
30
21810 N
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                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Than 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S23122; S23122.
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87 NFQLKHTGPG 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 30-58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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Gaps

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VARIANT VARIANT

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Length 207 2; Indels

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
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                (CYCLOPHILIN-1).

CYP-1 OR Y49A3A.5.

CYP-1 OR Y49A3A.5.

Eucanorhabditis elegans.

Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

NCBI_TaxID=6239;
                                                                                                                                                                                    Page A.P., Macniven K., Hengartner M.O.; "Cloning and blochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans."; Biochem. J. 317:179-185(1996).
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                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.4%; Score 45; DB 1; Length 192; 80.0%; Pred. No. 0.92; 1ve 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isomerase; Rotamase; Multigene family.
SEQUENCE 192 AA; 20710 MW; C2094D91809ECE85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, U30943; AAC47116.1; --.
EMBL, AL033512; CAA22075.1; --.
EMBL, AL033512; CAA22075.1; --.
WOFMSPED: Y49A3.4; CES213.
InterPro; IPR002130; CSA_PPIASG.
Pfam; PF00160; pro_isomerase; Pram; PR00163; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; IPROSITE; PS0072; CSA_PPIASE_1; I.
                                                                                                                    [1]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-96276416; Pubmed-8694762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 63.4
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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Search completed: January 15, 2002, 13:14:59 Job time: 655 sec

112 NFDLKHTGPG 121

g 9

1 NFKLKHYGPG 10

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; Search time 78.85 Seconds
(without alignments)
20.406 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries SPTREMBL\_17:\* Database :

sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp\_invertebrate:\*
sp\_manmal:\*
sp\_mhc:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\* sp\_organelle:\* sp\_rodent:\* sp\_plant:\* sp\_phage: \* 55: 77: 78: 10: 111: 113:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

O88541 rattus norv O9bvk5 homo sapien O9dcy1 mus musculu O9dcy1 mus musculu O917v3 drosophila O62190 caenorthabdi O9w27 drosophila O44073 tachypleus C29774 schistcosoma C29778 sus scrofa O95p0 arabidopsis O69p03 arabidopsis O91y53 arabidopsis O91y53 arabidopsis O91y64 arabidopsis O91y4 arabidopsis O91y4 arabidopsis O92515 arabidopsis O91y4 arabidopsis O60876 arabidopsis O60876 arabidopsis Description SUMMARIES 088541 09BVK5 0917V3 062190 09W27 044073 027774 02851 09SP02 02851 02651 02651 038867 09LYN4 022515 080876 040672 Query Match Length DB 216 120 204 205 205 220 213 213 234 1143 1176 1176 1176 1176 1000.0 1000.0 1000.0 188.7 888.7 888.7 775.1 775.1 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773.2 773 Score Result ٠ يو

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## ALIGNMENTS

RESULT

	PRELIMINARY; PRT; 208 AA.		(TrEMBLrel.	(TrEMBLrel.		8).	Rattus norvegicus (Rat).	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Eureleostomi.	Rodentia:			CE FROM N.A.	STRAIN-WISTAR-KYOTO; TISSUE-KIDNEY;	Kainer D.B., Doris P.A.;	philin B.";	Submitted (JUN-1998) to the EMBL/GenBank/DDB. darahases	FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCEPTED THE		CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE INIDIC	PEPTIDE BONDS IN OLIGOPEPTIDES.	SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-BROLY CIS-	TRANS ISOMERASE FAMILY.	EMBL; AF071225; AAC25590.1;	HSSP; P23284; 1CYN.	InterPro; IPR002130; CSA_pPlase.	Pfam; PF00160; pro_isomerase; 1.	PR00153; CSAPPISMRASE.	<pre>3; PS00170; CSA_PPIASE_1; 1.</pre>	PROSITE; PS50072; CSA_PPIASE_2; 1.	ise; Rotamase.	E 208 AA; 22802 MW; 02408DFA7157218C CRC64;	th 100.0%; Score 71; DB 11; Length 208; Similarity 100.0%; Pred No. 0 00012.	vative 0;	
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XREDLINE-21085660; PubMed-11217851;

XREDLINE-21085660; PubMed-11217851;

XRA ATARWAT, Shibata K., Yoshino M., Itoh M., Ishii Y.,

A ATARWAT, Izwam A., Shibata K., Yoshino M., Ttoh M., Ishii Y.,

A ATARWAT, Izwam M., Nishi K., Klyoswam H., Kondo S., Yamanaka I.,

A ATARWAT, Izwam M., Nishi K., Klyoswam T., Salto R.,

A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo W., Anon H., Baldarelli R., Barsh G.,

Sakai K., Okidor T., Furuno M., Anon H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Ra Brownstein M.J. Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Nordone P., Ring B., Riggwald M., Mazzarelli J., Mombaerts P.,

Ra Sasaki H., Sato K., Schoenbach C., Seya I., Shibata Y., Storch K.-F.,

Ra Sazaki H., Sato K., Schoenbach C., Seya I., Shibata Y., Storch K.-F.,

Ra Sazaki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Mynshwa-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinger_TaxID=10090;
                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
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Pred. No. 0.00012;
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
EMBL, BCO01125; AAH01125.1: -.
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Last annotation update)
                                                                                                                        01-JUN-2001 (TIEMBLEEL 17, Last Sequence update) 01-JUN-2001 (TIEMBLEEL 17, Last annotation update) PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B).
                                                                      216 AA
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EMBL; AK002357; BAB22036.1; -.
MGD; MGI:97750; Pplb.
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-SKIN, AND MELANOMA;
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                              Homo sapiens (Human).
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MEDLINE-20196006; Pubbed-10731122;

Radams M.D. Celniker S.E., Holt R.A., Bevans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W. Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W. Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer B.G., Li P.W., Honderson S.N.,
Sutton G.G., Wortnan J.R., Yandell W.D., Zhang G., Change W. Pfelffer B.D.,
RA Burtles R.W. Basud A. Baxenfalle J., Bayerkaroglu L., Baldwin D.,
RA Beson K.Y. Beacos P.V., Berman B.P., Bhandari D., Boslshakov S.,
Burtles R.C., Busam D.A., Buller H., Cadieu B., Center A., Chandra I.,
RA Burtles R.C., Busam D.A., Buller H., Cadieu B., Center A., Chandra I.,
RA Gerlos B., Delcier A., Deng R., Mays A.D., Dew I., Distas P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson R., Dougleiste C.C., Perraz C., Feritara S., Felschmann W.,
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RA Glodek A., Gong F. Gorrell J.H., Gu Z., Guun P., Harris N.L., Harvey D., Hehman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Woll M.-H., Ibeywan C.,
A Hostin D., Houston K.A., Howland T.J., Woll M.-H., Ibeywan C.,
A balail M., Kalush F., Karpen G.H., Kaz, Kanipan D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A kurmel B.E. Kodira C.D., Kraft C., Mortis J., Moshrefi A.,
Mount S.M. Moy M. Murphy B., Murphy L., Muzny D. M., Nelson D.,
RA Rhander K., Welson K.A., Nixon K., Morthes D., Caller B.,
Rainert K., Welson K.A., Nixon K., Wolfer E., Wang A.,
Rander K., Welson C. C., Turner R., Wanger B., Shen H.,
Rayirkas R., Pecchal C., Standers R.D.C., Scheeler F., Shen H.
Rayirkas R., Welchamos I., Singele C., Shen B.,
Rathilams S.M., Woodage T., Wolter E., Wang G., Zhan A., Zhang G., Zhan M., Zhang G., Zhan X., Zhan M., Zhang G., Zhan M., Zhang K.H., Zhang G., Zhan M., Zhang G., Zhan M., Zhang S., Zhu X., Zhan M., Shue B.C., Zhan M., Welcer C., Zhang W., Zhang S., Zhu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Eukaryota; Metazob; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidac; Drosophilla.

NCBL_TaxID=7227;
                                                                                                                                                                     Gaps
                                                                                                                                                                     ;
                                                                                                                           Length 216;
                                                                                                                                                                       Indels
Pfam; PF00160; pro_isomerase; 1.
PROSITE; PS0072; CSAPPISMEASE.
PROSITE; PS50072; CSAPISSE_2; 1.
SEQUENCE 216 AA: 23713 MW; CE9DAD1544AE72FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                           Score 71; DB 11;
Pred. No. 0.00012;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                  120 AA.
                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BERKELEY;
MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                          ö
                                                                                                                                100.0%;
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                                                                                                                                  Query Match 100.0
Best Local Similarity 100.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                           127 NFKLKHYGPGW 137
                                                                                                                                                                                                                    1 NFKLKHYGPGW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG2852 PROTEIN.
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0917V3
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Q9W227
                                       RESULT
                                                         09W227
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Caraton M., Dear S., Du Z., Dutbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightung J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Santh A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOLDING OF PROTEINS (BY SIMILARITY).
-:- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-:- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 368:32-38(1994).
-!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
                                                                                                                                                               :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63; DB 5; Length 204; Pred. No. 0.0029;
                                                                                                                     88.7%; Score 63; DB 5; Length 120; 90.9%; Pred. No. 0.0016; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cottage A.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isomerase; Rotamase.
SEQUENCE 204 AA; 21927 MW; 6216192BFE1FB493 CRC64;
                                                                      CF93898B694FA9F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                     204 AA.
                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                    PRT;
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                 Pfam: PF00160; pro_isomerase: 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE: PS50072; CSA_PPIASE_2: 1
SEQUENCE 120 AA: 12962 MW: CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002130; CSA_PPIase.
InterPro; IPR002130; CSA_PPIase
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90.98;
                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-JUN-2001 (TrEMBLrel. 17, CXP-5 PROTEIN (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z92784; CAB07192.1;
HSSP; P23284; 1CYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

Best Local Similarity 90.99
Matches 10; Conservative
                                                                                                                       Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                              1 NFKLKHYGPGW 11
                                                                                                                                                                                                                              27 NFKLKHYGAGW 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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062190
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RX AGABLA-ERREALEY;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

RA Amantides P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortunan J.R., Yandall N.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazal R.G., Clampe M., Pfeiffer B.D.,

RA Brandon R.C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,

Ballew R.M., Basu M., Baxendale J., Rayzaktaroglu L., Beasley E.M.,

Ballew R.M., Bolley P.V., Bernan B.P., Bandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Bortis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferricra S., Fleischman W.,

RA Bortis K.J., Evangelista C.C., Ferraz C., Ferricra S., Fleischman M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Gaba P., Harris M.,

Lasko P., Lei Y., Levitsky A.A., Li J.J., Mishian N., Nelson D.A.,

RA Minel B.E., Kodira C.D., Kraft C., Kratt C., Kratt E., Shon H.,

Ralush R.M., Murphy B., Murphy L., Murny D.M., Nelson D.,

Ralush R.M., Plance G.B., Pan S., Pollard J., Weissenbach J.,

Ralush R.M., Plance C.C., Prance R., Vollard J., Purt V., Wang X.,

Raber E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Syriskas R. W., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,

Raber E., Shradling R.C., Sunders R., Wood S., Zhon X., Smith H.S.,

Steps C., Share S., Rodiner E., Wang G., Zhon X., Smith R.,

Steps C., Shore S., Pan S., Pollard J., Pan S., Pollard J.,

Raber E., Spradling R.C., Staple
                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOLDING OF PROTEINS (BY SIMILARITY).
-:- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
                                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
205 AA.
                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPTIDE BONDS IN OLIGOPEPTIDES.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002130; CSA_PPIase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE003458; AAF46873.1; -. HSSP; P23284; 1CYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0034753; CG2852
                                            13,
13,
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  PRELIMINARY;
                                          (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=BERKELEY;
                                                                                                                                                                                                                    Ephydroidea; Dro
NCBI_TaxID-7227;
                                                                                                           CG2852 PROTEIN.
                                       01-MAY-2000
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Gaps

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1; Indels

Mismatches

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213 AA; 23238 MW;
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9551 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYCLOPHILIN B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                Query Match 77.5
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                   23
213
213
                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 NFKLKHVGAGW 130
                                                                                                                                                                                                                                                                                                                                                                                                                             1 NFKLKHYGPGW 11
                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                  NCBI_TaxID-6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9823;
                                                                     STRAIN-CHINESE;
                          Schistosoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
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                                                                                                                                                                        01-JUN-1998 (TTEMBLrel. 06, Created)
01-JUN-1998 (TEMBLrel. 06, Last sequence update)
01-JUN-2001 (TEMBLrel. 17, Last annotation update)
ROTAMASE, PROLYL CISTRANS ISOMERASE G PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN G) (P27),
Tachypleus tridentatus (Japanese horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Tachypleus.
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1999 (TERMELrel. 09, Last sequence update)
01-JUN-2001 (TEMELrel. 17, Last sequence update)
PEPTIOYL-PROLY CIS-TRANS ISOMERASE B PECCURSOR (EC 5.2.1.8) (PPIASE SPHISTOSOME B) (CYCLOPHILIN B) (S-CYCLOPHILIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                              Takaki Y., Muta T., Iwanaga S.,
"A peptidyl-prolyl cis/trans-isomerase (cyclophilin G) in regulated
georetory granules.",
J. Biol. Chem. 272:28615-28621(1997).
-i. FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS. MAY PLAY PROLE IN MAINTAINING THE CONFORMATIONAL INTEGRITY OF STORED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDYL-PROLYL CIS-TRANS ISOMERASE G. 728CB63EBB821C68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-1- ENZYME REGULATION: INHIBITED BY CYCLOSPORIN A (CSA).
-1- TISSUE SPECIFICITY: HEMOCYTE LARGE SECRETORY GRANDLES.
-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclosporin; Isomerase; Rotamase; Signal; Multigene family
                                 Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 63; DB 5; Length 220;
Pred. No. 0.0031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                      1: Indels
22199 MW; A9CEF88B1CC813F7 CRC64;
                                Score 63; DB 5;
Pred. No. 0.0029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 AA.
                                                                                                                                                           220 AA
                                                      0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AB002814; BAA23764 1;
HSSP; P23344; 1CV.
INTERPOO; IPR002130; CSA_PPT488-
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                            TISSUE-HEMOCYTE;
MEDLINE-98019238; Pubmed-9353327;
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24198 MW;
                                88.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.7%;
                               Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                           PRELIMINARY;
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                            Limulidae; Tachypleus.
NCBI_TaxID-6853;
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                                                                                         112 NFKLKHYGAGW 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 NFKLKHYGAGW 137
                                                                             1 NFKLKHYGPGW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NFKLKHYGPGW 11
¥¥;
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205
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SEQUENCE
SEQUENCE
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Q27774
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Eukaryota, Metazoa, Platyhelminthes, Rhabditophora, Neodermata;
Trematoda, Digenea, Strigeidida, Schistosomatoldea, Schistosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B. PREVENT SECRETION FROM ER (BY SIMILARITY).
D4986CDF7EDB8368 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Winteroe A.K., Fredholm M., Davies W.;
"Evaluation and characterization of a porcine small intestine cDNA library: analysis of 839 clones.";
Mamu. Genome 7:509-517(1996).
HSRP; P14628; CAA23162.1; -...
HSSP; P23284; ICYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutheria: Cetartiodactyla: Suina: Suidae: Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
Multigene family.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55; DB 5;
Pred. No. 0.073;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00160; Pro_isomerass: 1.
PRNINTS: PR00153; CSAPPISMRASE.
PROSITE: PS000770; CSA_PPIASE_1: 1.
PROSITE: PS500770; CSA_PPIASE_2: 1.
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                                                                                                                                                         MEDLINE-97053959; PubMed-8898338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-SMALL INTESTINE;
MEDLINE-96327607; Pubmed-8672129;
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002130; CSA_PPIase.
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EU Arabidopsis sequencing project;
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SEQUENCE FROM N.A.
                                                                                         NCBI_TaxID=6183;
                                                                               Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09LY53
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                                                                                                                                                                                                                                                                                                                                                                                          "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Pepermatophyta; Pagermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                        Gaps
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CY. WASSILEWSKIJA;
STRAIN-CY. WASSILEWSKIJA;
SACKSON K.M., SOLL D.;
"Mutations in a maphidopsis cyclophilin disrupt interaction with protein phosphatase 2A.";
                                                                                                                                                                                                                                                                                                                                                                                                               clones..;
-1731-6342000).
-18 ABA RES. 7.31-6342000).
-18 FUNCTION: PEPTIDYL. PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
-18 CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-18 SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                STRAIN-COLUMBIA;
MEDLINE-20181125; PubMed-10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
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 DB 6; Length 87;
0.043;
                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     026551 PRELIMINARY; PRT; 213 AA. 026551; 11-3AN-1999 (TrEMBLrel. 09, Created) 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.2%; Score 52; DB 10;
81.8%; Pred. No. 0.23;
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1; Mismatches
                                                                                                                      204 AA.
                     0; Mismatches
76.1%; Score 54; 100.0%; Pred. No.
                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                      PRT:
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PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF192490; AAF05760.1; -- EMBL, AA6020755; BAA97339.1; -- HSSP; P21284; ICYN. InterPro, IPR002130; CSA_PPIASE.
                                                                                                                                                                                                                                                                                                                 Mol. Gen. Genet. 0:0-0(1999).
                    B; Conservative
                                                                                                                     PRELIMINARY;
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Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 NFKLKHTGPGF 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NFKLKHYGPGW 11
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SEQUENCE FROM N.A.
         Best Local Similarity
                                          4 LKHYGPGW 11
                                                     1 LKHYGPGW 8
Query Match
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                                                                                                                              09SP02;
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                                                                                              10
                    Matches
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09SP02
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1441
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CYCLOPALIA and List expression in Bscherichia coli.";
MOL. Biochem. Parasitol. 75:99-111(1995).

-1. FUNCTION: PPIASES ACELERARE THE FOLDING OF PROTEINS.

-1. CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PETIDE BONDS IN OLIGOPETIDES.

-1. ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.

-1. DEVELOURMENTAL STRAGE: THIS SOLUBLE PROTEIN IS PRESENT IN ABUNDANCE
IN THE ADULT WORM AS WELL AS IN THE SCHISTOSOMULA AND THE EGGS.

-1. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FMAILY.
01-JUN-2001 (TremBirel, 17, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN),
                                                                                                                                                Metazou, Platyhelminthes, Rhabditophora, Neodermata,
Digenea, Strigeidida, Schistosomatoidea; Schistosomatidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae;
Burosids II; Brassicales; Brassicaceae; Arabidopsis.
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15FF6371E60B7415 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Cioli D., "Characterization of a Schistosoma mansoni cDNA encoding a B-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
Multigene family. 3 POTENWIAL.
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Benes V., Wurmbach E., Drzonek H., Ansorge W., Mewes H.W., Rudd
Lemcke K., Mayer K.F.X., Ouetier F., Salanoubat M.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                   Klinkert M.-O., Bugli F., Engels B., Carrasquillo E., Valle C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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Q0LY53;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN-LIKE PROPERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF00160; pro_isomerase; 1
PRNTWS: PR00153, CSAPPISHRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1
PROSITE; PS50072; CSA_PPIASE_2; 1
                                                                                                              Schistosoma mansoni (Blood fluke).
                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96362065; PubMed-8720179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002130; CSA_PPIase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U30874; AAC46985.1; -. HSSP; P23284; ICYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
213
213
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=PUERTO RICAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 NFKLRHVGAGW 130
                                                                                                                                          Eukaryota; Metazou;
Trematoda; Digenea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NFKLKHYGPGW 11
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SEQUENCE

Query Match

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025093 025093

SO DER REPORT OF THE PROPERTY 
13

RESULT Q25093

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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Pagnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPTIDE BONDS IN OLIGOPEPTIDES.
-1. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRNS ISOMERASE PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chou I.T., Gasser C.S.;
"Characterization of the cyclophilin gene family of Arabidopsis
"Characterization of the cyclophilin proteins.";
Haliana and phylogenetic analysis of known cyclophilin proteins.";
Plant Mol. Biol. 35:873-892(1997).
-i- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOLDING OF PROTEINS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18969 MW; 24C2031B6CA107A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                               (TremBirel, 01, Created)
(TremBirel, 01, Last sequence update)
(TremBirel, 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
0.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51;
Pred. No. (
                                                                                                                 (Mouse-ear cress).
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PRT;
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PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98088013; PubMed-9426607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.0,
                                                                                CYCLOPHILIN (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
PRELIMINARY;
                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isomerase; Rotamase.
SEQUENCE '176 AA;
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                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     STRAIN-LANDSBERG;
                                                                                                                                                                               NCBI_TaxID=3702;
                               01-NOV-1996
01-NOV-1996
01-JUN-2001
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038867;
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                                                                                                                                                                                                                                                                                                                         Gaps
          -:- FUNCTION: PEPTIDYL-PROINT CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
-:- CATALITIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-:- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-96167279; PubMed-8887897;
MCDINGEN S., Blackshaw S.E., Kaiser K., Davies J.A.;
MCDING Libraries from identified neurons.";
Proc. R. Soc. Lond., B. Blol. Sci. 263:57-62(1996).
-i- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN-A (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.24;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 AA.
                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR002130; CSA_PPIASE.
Pfam; PF00160; pro_ISOMETASe; 1.
PROSITE; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                 EMBL; ALIG8822; CABB?846.1; ...
InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 2.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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EMBL; U36797; AAB01531.1; -.
HSSP; P05092; 2CPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                       Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity
- Local 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                              155 NFKLKHTGPGF 165
                                                                                                                                                                                                                          Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rotamase.
                                                                                                                                                                                                                                                                                                                                                            1 NFKLKHYGPGW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NFKLKHYGPG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 NFKLKHTGPG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6421;
                                                                                                                                                                                                                           somerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (somerase;
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Gaps

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EMBL; U40400; AAB96833.1; -

SEQUENCE

RESULT 14

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038867

Length 176 1; Indels

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DR HSSP; P05092; ICWI.

DR Mendel; 6283; Arath;1040;6283.

DR InterPro; IPR0012330; CSA_PRISS.

DR Pfam; PP00150; Dro, isometrase; 1.

DR PROSITE; PR00153; CSA_PPISMRASE.

DR PROSITE; PS50072; CSA_PPIASE_1; 1.

DR PROSITE; PS50072; CSA_PPIASE_2; 1.

KW ISOMERASE; Rotamase.

SQ SEQUENCE 176 AA: 18906 WW; 24C2031B6BC4DD90 CRC64;
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Ouery Match
Best Local Similarity 90.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps
Oy 1 NFKLKHYGPG 10
Db 94 NFKLKHYGPG 103

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> Search completed: January 15, 2002, 13:16:26 Job time: 657 sec

